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(12) **United States Patent**
Becnel et al.(10) **Patent No.:** US 6,521,454 B1
(45) **Date of Patent:** Feb. 18, 2003(54) **BACULOVIRUSES, INSECTICIDAL COMPOSITIONS, AND METHODS FOR CONTROL OF INVERTEBRATES**(75) Inventors: **James J. Becnel**, Gainesville, FL (US); **Fukuda Tukuo**, Gainesville, FL (US); **Bettina Moser**, Gainesville, FL (US); **Andrew Cockburn**, Morgantown, WV (US); **Susan E. White**, Gainesville, FL (US); **Albert H. Undeen**, Whittier, NC (US)(73) Assignee: **The United States of America, as represented by the Secretary of Agriculture**, Washington, DC (US)

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(57) **ABSTRACT**

Although the present invention has been described with reference to specific details of certain embodiments thereof, it is not intended that such details should be regarded as limitations upon the scope of the invention except as and to the extent that they are included in the accompanying claims.

29 Claims, No Drawings

**BACULOVIRUSES, INSECTICIDAL
COMPOSITIONS, AND METHODS FOR
CONTROL OF INVERTEBRATES**

FIELD OF THE INVENTION

The invention relates to the fields of insect control using baculoviruses and control of baculoviral infections in invertebrates.

BACKGROUND OF THE INVENTION

Historically, mosquito control operations have primarily used chemical pesticides or the bacterium *Bacillus thuringiensis israelensis* (Bti) for control of larval mosquitoes. Chemical larvicides are rapidly losing market share due to safety issues and the expense of treating large aquatic habitats, where the larvae are produced. While Bti is effective and safe, it is quickly inactivated in the environment, and works poorly in polluted water habitats.

The other major biocontrol for insects is viruses, and the Baculoviridae family of viruses, commonly called baculoviruses, has been widely studied and developed commercially for certain insects. Baculoviruses are composed of large, double-stranded, circular DNA molecules that are packaged in rod-shaped capsids. The Baculoviridae includes the Nucleopolyhedroviruses and the Granuloviruses subgroups (see Granados R R and B A Federici, Eds. 1986 *The Biology of Baculoviruses*, Vol. 1. Boca Raton, Fla.: CRC Press; Volkman, L E et al. 1995. *Baculoviruses*. In: Virus Taxonomy. Sixth Report of the International Committee on Taxonomy of Viruses. Murphy, F A et al. Eds Springer Verlag Wien).

Insect control using baculoviruses is an attractive approach, because baculoviruses only infect invertebrates, and they can generally be produced in sufficiently high numbers for commercial use. The viruses are produced naturally in two forms: "occluded" and "non-occluded". The occluded form, in which the DNA genome is surrounded by crystalline proteins (forming a structure called the inclusion or occlusion body), is the form in which the virus is spread naturally from one insect to another. It is also the form that makes a good insecticide formulation, since it is stable in the environment and in commercial packaging, and it can be mixed more readily with other pesticide formulations.

Despite the many advantages of baculoviruses for insect control, one commercial disadvantage is that a single baculovirus species has a fairly narrow host range, so a given baculovirus cannot be used for broad spectrum insect control. One of the best studied baculoviruses, *Autographa californica* nuclear polyhedrosis virus (AcNPV), is considered to have a fairly broad host range for a baculovirus, since it is known to infect over thirty species of Lepidoptera. The celery looper multiple embedded virus described by Hostetter and Puttler (U.S. Pat. No. 4,911,913) also is considered to have broad insecticidal activity within the Lepidoptera.

Thus, to develop an effective baculoviral control strategy for mosquitoes, there is a need to identify a viral strain that will infect as many mosquito species as possible. The first documented report of a mosquito pathogenic virus was made in 1963 with the discovery of a "cytoplasmic polyhedrosis virus" from *Culex tarsalis* in California (Kellen et al., 1963, J. Insect Pathol. 5:98–103), but this virus was later shown to be a densonucleosis virus, from the family Parvoviridae (Federici, B A 1985, "Viral Pathogens". IN Biological Control of Mosquitoes, H C Chapman, Ed., Bull. No. 6, American Mosquito Control Association, Inc., pp. 62–74).

Additional viruses pathogenic to mosquitoes have been reported from many different mosquito hosts, primarily by researchers in the U.S., Europe and Russia (Federici, 1985; ibid.; Goettel, M S 1985 Agr. Forestry Bull. 8:41–44). The first report of a baculovirus from a mosquito host was from *Aedes sollicitans* collected in Louisiana (Clark, T B, H C Chapman, and T Fukuda, 1969, J. Invert. Pathol. 14(2):284–286). Natural infections with NPVs have been reported from about ten mosquito species representing the genera *Aedes*, *Anopheles*, *Culex*, *Psorophora*, *Uranotaenia* and *Wyeomyia* (Federici, ibid.). Such infections were identified as being NPV infections based only on electron microscopic observations of the shape and size of occlusion bodies in collected larvae and on histopathological and cytopathological observations on infected larvae (Federici and Lowe 1972 Invert. Pathol. 20:14–21; Federici, B A 1980 Virology 100: 1–9; Stiles and Paschke 1980 J. Invertebr. Pathol. 35: 58–64). The AesoNPV characterized by these researchers produces spindle-shaped occlusion bodies 5–20 microns in length. H. Chapman (1974, Ann Rev Entomol 19:33–59) characterized an NPV infection in *Culex quinquefasciatus* in which the occlusion bodies are globular and from 1–5 microns in diameter. A viral disease of *Culex tarsalis*, characterized by tetragonal inclusion bodies, was described by W. R. Kellen et al. (1963, J. Insect Pathol. 5:98–103). While this virus was lost upon culturing, Clark and Chapman concluded it was the same virus that infected *Culex salinarius* (1969, J. Invert. Pathol 13:312), a virus that did not infect *Culex peccator* or *Culex quinquefasciatus*.

This area of mosquito pathology has received very little attention since these preliminary, initial reports 25–30 years ago, despite the tremendous advancements made with other insect baculoviruses for use as biopesticides and expression vectors (Adams, J R and J T McClintock, 1991, pp. 87–204 In: *Atlas of Invertebrate Viruses*, Adams and Bonami, Eds., Boca Raton: CRC Press; Possee, R D 1997, Curr. Opin. Biotechnol. 8: 569–572; and Possee, R D et al. 1997 Pestic. Sci. 51: 462–470), and no NPV has been purified or isolated from mosquitoes to allow molecular studies for unequivocal identification. A major reason for the inactivity in this area has centered on the inability to reliably transmit mosquito baculoviruses to their original and alternate hosts (Federici, 1985). There are numerous factors that can affect the infectivity of a baculovirus for an insect host, including chemical, physical and/or biological factors.

Much effort has been directed at developing methods and protocols to enhance the storage and stability of baculoviruses (usually in occluded form), for use in field applications. Factors that either reduce or enhance infectivity have been identified as components of storage mixtures, formulations, or crops on which baculoviral applications are to be made. For example, several proteins have been shown to enhance baculoviral infections. Enhancin, a metalloproteinase, has been isolated from an armyworm (*Trichoplusia ni*) granulosis virus (GV), and it can enhance the activity of baculoviruses by digesting certain peritrophic membrane proteins (Corsaro et al. 1993, In "Parasites and Pathogens of Insects", Beckage, N E et al., Eds., Volume 2: pp. 127–145, Academic Press, San Diego; Lepore L S. et al. 1996 J. Invertebr. Pathol. 68(2): 131–140; Wang P and R R Granados 1997, Proc. Natl. Acad. Sci. USA 94(13): 6977–6982; Wang, P. et al. 1997 J. Gen. Virol. 78: 3081–3089). A virus enhancing protein has also been detected in the spheroid, spindle and virion of an entomopoxvirus (Wijonarko A and T Hukuhara 1998, J. Invertebr. Pathol. 72(1): 82–86). Chitinase has also been shown to enhance infectivity of the gypsy moth NPV (Shapiro M et al.

1987, J. Econ. Entomol. 80(6): 1113–1116). Several acids, including boric and sorbic, have been shown to enhance infectivity of lepidopterous baculoviruses (Morales L et al. 1997, Ann. Soc. Entomol. Bras. 26(1): 115–120; Shapiro M and R A Bell 1982, Ann. Entomol. Soc. Am 75(3):346–349), while tannic acids have been shown to inhibit NPV infectivity (Keating et al. 1989, J. Invertebr. Pathol. 54(2):165–174; Young et al. 1995, Biological Control 5(2): 145–150).

Studies investigating the effects of various plant constituents on the infectivity of baculoviruses found that most of these actually inhibit infectivity (Elleman C J and Entwistle P F 1985, Ann. Appl. Biol. 106(1): 83–92, 93–100; Felton G W and S S Duffey 1990, J. Chem. Ecol. 16(4): 1221–1236; Hoover K et al. 1998 J. Chem. Ecol. 24(2): 253–271; Keating, S T et al., 1990 J. Invertebr. Pathol. 56(3): 317–326).

In addition to the use of naturally occurring baculoviruses as insect control agents, it is possible to improve the insecticidal capabilities of such baculoviruses by engineering the virus so that it is more aggressive in killing its host, which is not typically the goal of a natural viral infection. By improving the rate of killing, the engineered baculoviruses limit the feeding and consequently damage caused to crops. Since farmers tend to apply insecticides only when damage becomes visible, it is important that the insecticide act swiftly. For example, Miller and O'Reilly have described a mechanism of improving the LT_{50} (the time needed to kill 50% of the insect population) by deleting a gene which causes the production of an enzyme that inactivates insect molting hormones, ecdysteroid UDP-glucosyl transferase (EGT) (U.S. Pat. No. 5,352,451). The expression of the baculovirus EGT gene in wild-type baculoviruses prevents the insect larva from molting or pupating, allowing more time for the virus to propagate itself in the larval stage. Inactivation of the baculovirus EGT gene allows molting and pupation of the infected larva to proceed, which results in a shorter larval stage and less damage to crops. As another example, Hammock et al. (U.S. Pat. No. 5,674,485) have shown that juvenile hormone esterase can also be used in recombinant baculoviral insecticides to improve the LT_{50} .

Several authors have described techniques and methods for engineering insect toxin protein genes into the baculoviral genome, providing for exposure of the insect to not only an infectious virus particle but additionally to a debilitating toxic molecule, such as polypeptide toxins produced by scorpions, wasps, mites, or spiders. Tomalski et al., U.S. Pat. No. 5,266,317, issued Nov. 30, 1993, describe the use of recombinant baculoviruses that express an insect-specific paralytic neurotoxin of an insect predaceous mite. Additionally, insect-selective toxins have been identified in venoms from snails, spiders, and a number of other arthropods (see review by Zlotkin, 1985, In Comprehensive Insect Physiology, Biochemistry, and Pharmacology, Vol. 10, Chapter 15, pp. 499–541). The use of more than one toxin gene in a recombinant baculovirus has also been described, to maximize the insect-killing rate and to minimize the chance for resistance to develop (U.S. Pat. No. 5,756,340 Hammock, et al.).

There remains a need to identify methods for effective transmission of baculoviruses to mosquitoes in the environment. There also remains a need to provide improved baculovirus compositions for enhanced transmission of baculoviruses to insects in the environment.

SUMMARY OF INVENTION

This invention provides an insecticidal composition comprising (a) a baculovirus effective for producing a lethal or

debilitating infection in an insect; and (b) at least 1 mM of a divalent cation selected from the group consisting of: magnesium, cobalt, strontium and nickel is disclosed. Also provided are methods for controlling insect pests comprising the step of applying an insect-controlling amount of the composition to a habitat for the insect pests.

This invention further provides novel, isolated mosquito-infecting baculoviruses having at least one of the following characteristics: (a) nuclear occlusion bodies, globular in shape, diameter approximately 400 nm, each containing between 1–8 rod-shaped virions, approximately 200×40 nm; (b) nuclear occlusion bodies with no surrounding membrane and with a density of approximately 1.14–1.18 g/ml which agglutinate upon freezing; and (c) infectious in *Culex quinquefasciatus* and *Culex nigripalpus*. The novel mosquito baculoviruses of this invention can also be characterized by nucleic acid sequences provided herein, as well as by polypeptides encoded by the nucleic acid sequences. Methods for the *in vitro* propagation of mosquito baculoviruses comprising infecting a culture of mosquito cells with the mosquito baculovirus, growing the cells in culture medium containing at least 1 mM of a divalent cation selected from the group consisting of: magnesium, cobalt, strontium and nickel and a chelator or binder that selectively reduces the effective calcium ion concentration below 1 mM until inclusion bodies are detected in the cells, and harvesting the virus from the cells, are also provided.

Other aspects of the invention comprise isolated nucleic acids of the novel mosquito baculoviruses, isolated nucleic acids encoding polypeptides of the novel mosquito baculovirus, and cells containing these nucleic acids.

Also provided are methods for controlling baculovirus infections in invertebrates comprising administering to invertebrates calcium, iron or copper ions to provide an effective concentration of at least 1 mM.

DETAILED DESCRIPTION OF THE INVENTION

Definitions

“Baculovirus” means a member of the family Baculoviridae, whether currently known or described in the future.

“CuniNPV” means a novel baculovirus that infects *Culex nigripalpus*.

“Insect-antagonistic gene” means any gene, the product (which may be anti-sense nucleic acid or a polypeptide) of which interferes with the growth, development, or reproduction of an insect. Examples of insect-antagonistic genes include toxins, insect hormones, insect hormone mimics, and sterilization peptides.

Detailed Description

Described herein is the discovery of improved insecticidal compositions for the control of insects using viruses of the Baculoviridae. The invention described herein includes a baculovirus-based insecticidal composition comprising (a) a baculovirus effective for producing a lethal or debilitating infection in an insect, and (b) at least 1 mM of a divalent cation selected from the group consisting of: magnesium, cobalt, strontium and nickel. In a preferred embodiment, the composition further comprises an insecticidal composition-suitable carrier. The baculovirus of the invention is any virus of the family Baculoviridae, previously known or hereafter isolated and described. As currently classified, the Baculoviridae consists of double-stranded, circular, closed DNA viral genomes (between approximately 80 and 230 kilobases) that are typically packaged in rod-shaped capsids,

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with a general size range of approximately 30–60 nanometers by 250–300 nanometers (Miller, L 1996 “Insect Viruses” In Fundamental Virology, 3rd Ed., Fields B N et al eds., Lippincott-Raven Publ., Philadelphia, Pa. USA). The existing genera and species in the Baculoviridae are listed in Virus Taxonomy—6th Report of the International Committee on Taxonomy of Viruses, Murphy F A et al. eds., Springer Verlag, Wien, 1995, pp 104–111. Baculoviruses are currently known to infect insects of the Lepidoptera, Coleoptera, Hymenoptera and Diptera, including but not limited to *Autographa californica*, *Heliothis zea*, *Heliothis armigera*, *Syngrapha falcifera*, *Spodoptera frugiperda*, and *Thichoplusia ni* (a complete list of hosts for known baculoviruses is provided in the Virus Taxonomy reference cited above). New members of the Baculoviridae are continually being discovered, and the compositions and methods of this invention are fully applicable to baculoviruses discovered in the future.

A lethal or debilitating infection in an insect is an infection in the larval stage which prevents the majority of adults from emerging, or in the cases where the adult emerges, in which the adult reproductive capacity is statistically significantly diminished. The divalent cation to be included in the composition can be Mg⁺⁺. Alternatively, Co⁺⁺, Sr⁺⁺ or Ni⁺⁺ can be used. In a preferred embodiment in a liquid formulation, at least 5 mM Mg⁺⁺ is used. No upper limit of the divalent cation, e.g. Mg⁺⁺ need be specified so long as the amount used is not toxic. For example, between 5 and 40 mM Mg⁺⁺ can be used. Alternatively, a combination of divalent ions comprising Mg⁺⁺ and one or more of the ions Co⁺⁺, Sr⁺⁺ or Ni⁺⁺, giving a total divalent concentration of at least 1 mM and preferably at least 5 mM, can be used. When used in a non-liquid formulation, the amount of divalent cation should be calculated on a weight/weight basis, i.e. 5 mM MgCl₂ would be approximately 1 g MgCl₂ per kg or liter of the formulation.

In a specific embodiment, the baculovirus-based insecticidal composition further comprises a chelator or binder that selectively reduces the effective calcium ion concentration below approximately 1 mM. In specific embodiments, the chelator or binder reduces the effective calcium ion concentration below approximately 0.5 mM or below 0.1 mM.

In another embodiment, the invention is a mosquito larvacidal composition comprising (a) a baculovirus effective for producing a lethal or debilitating infection in mosquito larvae; and (b) at least 1 mM of a divalent cation selected from the group consisting of: magnesium, cobalt, strontium and nickel. In a preferred embodiment, the composition further comprises a larvacidal composition-suitable carrier.

In preferred embodiments, the mosquito larvacidal composition comprises a baculovirus selected from the group of nuclear polyhedrosis viruses that infect Culex, Aedes, Anopheles, Psorophoia, Uranotaenia, and Wyeomyia mosquito species. In specific embodiments, the baculovirus can be AesoNPV or the novel baculovirus CuniNPV further described hereinbelow. In a specific embodiment, the composition is a preparation of air-dried, baculovirus-infected mosquito larvae that are processed into a powder containing at least 1 mM of a divalent cation selected from the group consisting of: magnesium, cobalt, strontium and nickel.

In other embodiments, the mosquito larvacidal composition further comprises a chelator or binder that selectively reduces the effective calcium ion concentration below approximately 1 mM. In specific embodiments, the chelator or binder reduces the effective calcium ion concentration below approximately 0.5 mM or below 0.1 mM.

Given the effectiveness of divalent cations, particularly Mg⁺⁺, in combination with the novel mosquito baculovirus of this invention, in enhancing baculovirus infectivity of mosquitos, it is possible to use this combination to enhance the infectivity of other agents, e.g. bacteria or other viruses, in mosquitos. Thus, in another embodiment, the mosquito larvacidal composition comprises (a) a microorganism or virus capable of producing a lethal or debilitating infection in mosquito larvae; (b) a mosquito baculovirus; and (c) at least 1 mM of a divalent cation selected from the group consisting of: magnesium, cobalt, strontium and nickel. In specific embodiments, the microorganism can be a bacterium or a fungus, the virus can be any mosquito-infecting virus, and the mosquito baculovirus is CuniNPV (as described herein). In a further embodiment, the composition further comprises a larvacidal composition-suitable carrier. In other embodiments, the mosquito larvacidal composition further comprises a chelator or binder that selectively reduces the effective calcium ion concentration below approximately 1 mM. In specific embodiments, the chelator or binder reduces the effective calcium ion concentration below approximately 0.5 mM or below 0.1 mM.

Generally, the insecticidal or larvacidal compositions can be in the form of: wettable powders, dispersible granular formulations, granules, suspensions, emulsions, solutions for aerosols, baits and other conventional insecticide preparations. Carriers for insecticidal compositions are well-known in the art and one of skill in the art can choose an appropriate carrier based on the application site and the target insect. Examples of techniques for the formulation of baculoviruses as insecticidal compositions are described in Rhodes D J (1993, “Formulation of Biological Control Agents” In Exploitation of Microorganisms; Jones D G ed., Chapman & Hall, London, pp. 411–429) and references cited therein. The insecticidal composition-suitable carrier can be a solid or liquid diluent or carrier. The diluent or carrier can be a liquid, such as water, alcohol, hydrocarbons or other organic solvents, or a mineral, animal or vegetable oil, or a solid, such as a powder, e.g. talc, clay, silicate or corn cob grits. Wetting agents, coating agents, agents to promote physical flexibility, UV protectants, dispersants and sticking agents can also be added to the insecticidal compositions of the present invention. Similarly, nutrients may be added to increase feeding behavior and/or to attract insects. Flow agents, for example, clay-based flow agents, may be added to minimize caking of the wettable powders or other dry preparations during storage. Alternatively, the insecticidal or larvacidal composition can be microencapsulated using plant lignins or other suitable microencapsulating materials as the carrier.

In any insecticidal or larvacidal composition of the invention, the baculovirus can be a recombinant baculovirus that has been engineered to express one or more insect-antagonistic genes. The insect-antagonistic gene can be any gene that interferes with the growth, development or reproduction of the insect. Such an engineered baculovirus is more aggressive in killing its host. By improving the rate of killing, such engineered baculoviruses may limit the number of subsequent generations of the insect that are produced, limit the opportunity for disease-causing viruses vectored by the insect to increase in number, and limit the potential for insects to develop resistance to the gene. In specific embodiments, the insect-antagonistic gene is selected from the group consisting of: scorpion toxins, straw itch-mite toxin, spider toxins, snail toxins, insect hormones, insect hormone mimics, sterilization peptides. However, it is recognized that it may not always be advantageous to improve

the rate of killing of the insect. For example, in the case of mosquito larvae, a slower kill rate may be advantageous because it maintains competition for nutrients and space against noninfected larvae.

Recombinant baculoviruses can be made using techniques well-established in the art. Generally, the recombinant baculovirus may be prepared by cloning a gene encoding the insect-antagonistic gene into a baculovirus transfer vector at a restriction site downstream of a promoter capable of directing expression of the insect-antagonistic gene in insect cells, and co-transfected cells susceptible to baculovirus infection with the recombinant transfer vector and an intact wild-type baculovirus DNA. Homologous recombination occurs, resulting in a recombinant baculovirus harbouring the chimeric gene operably linked to a promoter (U.S. Pat. No. 5,166,317). The recombinant baculovirus may or may not contain an expressible polyhedrin gene. When an expressible polyhedrin gene is provided, the occluded form of the virus is produced. Alternatively, those of routine skill in the art can construct recombinant, occluded baculoviruses by coinfection of cells with a helper virus which supplies polyhedrin gene function. The construction of a stable, occluded recombinant nuclear polyhedrosis virus which has a functional polyhedrin gene and which, in insect cells infected therewith, expresses an insect-antagonistic gene which is secreted by the cells, the insect-antagonistic gene product being expressed with a signal peptide such that the insect-antagonistic gene product is secreted from the insect cells is described in U.S. Pat. No. 5,770,192.

The present invention also provides methods for controlling insect pests comprising the step of applying an insect-controlling amount of the insecticidal compositions of this invention to a habitat for the insect pest. The insect-controlling amount is the amount sufficient to interfere with the growth, development and/or reproduction of the insect. The insect controlling amount can readily be determined experimentally by a person of ordinary skill in the art using bioassays and other information available in the art, examples of which are described herein.

Also disclosed and claimed herein are specific methods for controlling mosquitoes comprising the step of applying a mosquito-controlling amount of a mosquito larvacial composition to a habitat of mosquitoes. The amount to be applied can be in a liquid or non-liquid formulation. The formulation is chosen to maximize exposure of the target mosquito population to the larvacial composition by conventional application methods. Since mosquito larvae are filter feeders, the method of delivery is by ingestion. Delivery can be enhanced by the addition of feeding stimulants. In a preferred embodiment, the virus and sufficient Mg⁺⁺ are microencapsulated for delivery together to the mosquito gut. Encapsulation methods are well-documented in the art. Encapsulation of baculoviral-based insecticides helps to maintain activity by protecting the virus from harmful environmental conditions. Starch, flour and gluten have been studied extensively as materials to encapsulate insecticides. Such encapsulated insecticides can be applied as granular or sprayable formulations. Shasha et al. (U.S. Pat. No. 5,750,467) describe dispersible encapsulations or adjuvants that use plant lignins to deliver insecticides, such as baculoviruses. Lebo, Jr. et al. (U.S. Pat. No. 5,552,149) describe methods for microencapsulation such as pesticides that employ lignosulfonates, especially to provide protection from ultraviolet rays. The mosquito-controlling amount is the amount sufficient to interfere with the growth, development and/or reproduction of the mosquito larvae. In a specific embodiment, the habitat to which the larvacial

composition is applied is a mosquito breeding area, e.g. a body of water. In a specific embodiment, the mosquitoes to be controlled are members of the Culicidae.

The invention herein described further comprises a newly isolated mosquito-infecting baculovirus, hereinafter referred to as a CuniNPV, that is characterized by one or more of the following:

- (a) nuclear occlusion bodies, globular in shape, diameter approximately 400 nm (e.g. ± 10 nm), each containing between 1–8 rod-shaped virions, approximately 200× 40 nm;
- (b) nuclear occlusion bodies, with no surrounding membrane, with a density of approximately 1.14–1.18 g/ml which agglutinate upon freezing, and
- (c) infectious in *Culex quinquefasciatus* and *Culex nigripalpus*.

The isolated mosquito-infecting baculovirus can be further characterized by the presence of major occlusion body proteins, sized as 29.7 kDa and 97 kDa on SDS-PAGE.

Alternatively, the novel mosquito-infecting baculovirus of this invention can be characterized as a baculovirus which contains nucleic acid that shares at least 60% identity with the sequence of one or more nucleic acids selected from the group of sequences set forth as SEQ ID NO:1; SEQ ID NO:4; SEQ ID NO:10; SEQ ID NO:19; SEQ ID NO:38; SEQ ID NO:42; SEQ ID NO:44; SEQ ID NO:46; SEQ ID NO:48; SEQ ID NO:50; SEQ ID NO:53; SEQ ID NO:61; SEQ ID NO:66; SEQ ID NO:70; SEQ ID NO:72; SEQ ID NO:74; SEQ ID NO:76; SEQ ID NO:80; SEQ ID NO:83; SEQ ID NO:87; SEQ ID NO:94; SEQ ID NO:106; SEQ ID NO:117; SEQ ID NO:130; SEQ ID NO:145, and SEQ ID NO:146. In preferred embodiments, the novel mosquito-infecting baculovirus of this invention can be characterized as a baculovirus which contains nucleic acid that shares at least 70%, 80% or 90% identity with the sequence of one or more nucleic acids selected from the group of sequences set forth as SEQ ID NO:1; SEQ ID NO:4; SEQ ID NO:10; SEQ ID NO:19; SEQ ID NO:38; SEQ ID NO:42; SEQ ID NO:44; SEQ ID NO:46; SEQ ID NO:48; SEQ ID NO:50; SEQ ID NO:53; SEQ ID NO:61; SEQ ID NO:66; SEQ ID NO:70; SEQ ID NO:72; SEQ ID NO:74; SEQ ID NO:76; SEQ ID NO:80; SEQ ID NO:83; SEQ ID NO:87; SEQ ID NO:94; SEQ ID NO:106; SEQ ID NO:117; SEQ ID NO:130; SEQ ID NO:145, and SEQ ID NO:146. In specific embodiments, mosquito-infecting baculoviruses of this invention comprise a nucleic acid sequence with at least 75%, 77%, 79%, 81%, 83%, 85%, 87%, 89%, 91%, 93%, 95%, 97% or 99% identity to a nucleic acid selected from the group of sequences set forth as SEQ ID NO:147 and SEQ ID NO:148.

An example of a CuniNPV has been deposited with the American Type Culture Collection (10801 University Boulevard, P.O. Box 1549, Manassas, Va. 20108) under the Budapest Treaty on the International Recognition of the Deposit of Microorganism for the Purposes of Patent Procedure, on Feb. 3, 1999 as accession number VR-2639. The genome sequence of VR-2639 is deposited in GenBank under Accession Number AF403738.

An isolated mosquito-infecting baculovirus is one which has been either purified from infected mosquito larvae, cloned through plaque purification in mosquito cell culture, or otherwise prepared from a single viral isolate. A method for isolating the novel baculoviruses of this invention from infected mosquito larvae is described in the Examples.

Additional mosquito-infecting baculoviruses of this invention can be identified by probing viral DNA isolated from diseased mosquito larvae, obtained as herein described. One method for detection is the use of polymerase chain

reaction amplification. Polymerase chain reaction (PCR) amplification can be used to detect other mosquito-infecting baculoviruses of this invention by amplifying baculoviral specific DNA sequences. Repeated cycles of denaturation, primer annealing and extension carried out with polymerase, e.g., a heat stable enzyme Taq polymerase, lead to exponential increases in the concentration of desired DNA sequences. Using the nucleic acid sequences of a mosquito baculovirus as disclosed herein, synthetic oligonucleotides, or "primers", can be prepared which are complementary to the ends of sequences which are to be amplified. The sample DNA, obtained from mosquito larval populations, can be denatured at high temperatures (e.g., 95° C.) and then reannealed in the presence of a large molar excess of the primers. The primers, oriented with their 3' ends pointing towards each other, hybridize to opposite strands of the target sequence and prime enzymatic extension along the nucleic acid template in the presence of the four deoxyribonucleotide triphosphates. The end product is then denatured again for another cycle. After this three-step cycle has been repeated several times, amplification of a DNA segment by more than one million-fold can be achieved.

Primers chosen for the PCR amplification should be at least approximately 10 nucleotides in length and amplifying a product at least approximately 30 nucleotides in length. The length and G+C content of the primers are used to determine the melting temperature (T_m) according to formulas known in the art. The T_m establishes the temperature at which primer annealing to the sample DNA is performed. For primers shorter than 20 nucleotides, an estimate of T_m can be calculated as $T_m=4(G+C)+2(A+T)$, while for longer primers, an estimate of the T_m requires the use of the nearest neighbor calculation, which takes into account thermodynamic parameters and is embedded in most available computer programs for designing PCR primers (see, e.g. Dieffenbach, C S et al. 1995 General concepts for PCR primer design. IN: PCR Primer, A Laboratory Manual; Dieffenbach and Dveksler, eds., Cold Spring Harbor Laboratory Press, Plainview, N.Y.).

Detection of the amplified product can be by any of several standard methods, such as electrophoresis on an agarose or polyacrylamide gel and ethidium bromide staining to visualize the nucleic acids on the gel. Once the presence of a baculovirus in the sample has been detected, the novel mosquito-infecting baculovirus can be isolated and purified according to methods described herein.

The novel mosquito-infecting baculoviruses of the present invention can be propagated and produced by repeatedly infecting mosquito larvae and harvesting the larvae. Alternatively, the novel mosquito-infecting baculoviruses of the present invention can be propagated by introducing the baculovirus to a cultured mosquito cell, growing the mosquito cells for a period until inclusion bodies are detected inside the cells and then harvesting the baculovirus from the cells. Methods for culturing mosquito cells have been described (see, e.g. Kurtti and Munderloh 1984 Adv. Cell Cult. 3:259–302; Oelofsen, M J et al. 1990 J. Med. Entomol. 27:939–944; Charpentier, G et al. 1995 J. Med. Entomol. 32:793–800). In a specific embodiment, the mosquito cell culture medium for propagating the virus contains at least 1 mM divalent cation and less than 1 mM, Ca⁺⁺. In a preferred embodiment, the mosquito cell culture medium contains at least 5 mM Mg⁺⁺ and less than 1 mM, and preferably less than 0.5 or 0.1 mM, Ca⁺⁺.

Mosquito-infecting baculoviruses of this invention with significant homology, i.e. sequence identity, to one or more nucleic acids selected from the group of sequences set forth

as SEQ ID NO:1; SEQ ID NO:4; SEQ ID NO:10; SEQ ID NO:19; SEQ ID NO:38; SEQ ID NO:42; SEQ ID NO:44; SEQ ID NO:46; SEQ ID NO:48; SEQ ID NO:50; SEQ ID NO:53; SEQ ID NO:61; SEQ ID NO:66; SEQ ID NO:70; SEQ ID NO:72; SEQ ID NO:74; SEQ ID NO:76; SEQ ID NO:80; SEQ ID NO:83; SEQ ID NO:87; SEQ ID NO:94; SEQ ID NO:106; SEQ ID NO:117; SEQ ID NO:130; SEQ ID NO:145, and SEQ ID NO:146 can readily be obtained by screening collected mosquito larvae suspected of being infected with a probe comprising one or more nucleic acid sequences contained in SEQ ID NO:1; SEQ ID NO:4; SEQ ID NO:10; SEQ ID NO:19; SEQ ID NO:38; SEQ ID NO:42; SEQ ID NO:44; SEQ ID NO:46; SEQ ID NO:48; SEQ ID NO:50; SEQ ID NO:53; SEQ ID NO:61; SEQ ID NO:66; SEQ ID NO:70; SEQ ID NO:72; SEQ ID NO:74; SEQ ID NO:76; SEQ ID NO:80; SEQ ID NO:83; SEQ ID NO:87; SEQ ID NO:94; SEQ ID NO:106; SEQ ID NO:117; SEQ ID NO:130; SEQ ID NO:145, and SEQ ID NO:146, or a unique fragment thereof. Nucleic acid samples from collected mosquito larvae that specifically hybridize with such a probe under relatively high-stringency conditions (e.g. low salt conditions and/or high temperatures of hybridization) can be processed for the isolation of a mosquito-infecting baculovirus of this invention according to the procedures described herein.

As is known in the art, annealing reactions (between primers or probes and the sample DNA or RNA) are affected by the concentration, sequence complexity, base composition and length of the primer/probe; the concentration of monovalent cations; the presence of hybrid destabilizing agents (e.g. formamide); and the incubation temperature. The following formula relates many of these parameters to the T_m (the temperature at which half of the DNA molecules have dissociated into single strands): $T_m=81.5^\circ\text{C}+16.6 \log M+41$ (mole fraction of G+C)–(500/L)–0.62 (% formamide), where M is the molar concentration of monovalent cations and L is the molecular length of the probe DNA in bases. Increasing the salt concentration from 100 mM to 1 M increases the T_m by 16° C. Annealing temperatures that are 25° C. below the T_m of the native DNA usually provide the maximum rate of hybridization. For example, for genomic DNAs, the annealing temperature is typically 65° C. in aqueous solvents containing 250 mM Na⁺. Adding formamide to a final concentration of 50% lowers the annealing temperature to 42° C. In general, the higher the probe concentration, the more rapid the annealing reaction. However, the competing reaction of probe strands reannealing to each other will also occur more rapidly. For this reason, probe concentrations need to be kept relatively low (≤ 10 ng/ml hybridization solution). Alternatively, single-stranded probes can be used.

Stringency, or the degree to which mismatches are permitted in the binding of two single strands, is a critical parameter in all annealing reactions and is affected by salt concentration and annealing temperature. The T_m of a duplex decreases by approximately 1° C. for each 1% of mismatched base pairs, except for short DNA (15–30 bases, for which each mismatch can reduce the Tm by 5° C. (Wolff, R and Gemmill, R 1997 Purify and analyzing genomic DNA IN: Genome Analysis—A Laboratory Manual, Vol. 1; Birren, B et al., eds., Cold Spring Harbor Laboratory Press, Plainview, N.Y.). The higher the salt concentration, the greater the number of mismatches that can be tolerated at a given temperature. The final stringency of the reaction can then be readily adjusted by using a series of post-hybridization washes of increasing stringency. The specific hybridization signal should be assessed by autoradiography between these washes and compared with the background.

Several standard hybridization conditions have been developed on the basis of the considerations above. Stringent hybridization can be performed in an aqueous hybridization solution containing 2xSSC at 65° C. General methods for optimizing and performing hybridizations are set forth in Sambrook et al., "Molecular Cloning, a Laboratory Manual," Cold Spring Harbor Laboratory Press (1989). Any viruses so isolated can be confirmed to be a mosquito-infecting baculovirus of this invention by performing the biochemical/molecular, microscopic and infectivity characterizations described herein.

The novel baculoviruses of this invention can be engineered to express an insect-antagonistic gene under the control of a baculoviral promoter in amounts sufficient to produce a debilitating effect in the mosquito, for example paralysis or premature molting.

In one embodiment, a recombinant mosquito baculovirus can be constructed by inserting the promoter/insect-antagonistic gene at a location in the mosquito baculovirus genome that is a nonessential region for viral replication and propagation, by methods known to those skilled in the art. For example, the baculoviral genes identified as EGT, p10, DA26, ETL, p94 and orf603 have been shown previously to be good sites for insertion of an engineered promoter/insect-antagonistic gene construct. The egt gene in baculoviruses is typically located adjacent to the late expression factor 1 (lef-1) gene (SEQ ID NO:147, also present at nucleotides 2630–3334 in SEQ ID NO:13). The p10 gene is typically located immediately upstream of and in opposite orientation to the p74 gene (SEQ ID NO:148; also present at nucleotides 222–1253 in SEQ ID NO:66).

In a specific embodiment, the promoter/insect-antagonistic gene is inserted into the non-essential gene locus, by first constructing a transplacement, or transfer, plasmid which contains the desired promoter/insect-antagonistic gene flanked by CuniNPV non-essential gene sequences, and all the elements necessary for autonomous replication in bacteria, such as *E. coli*. Such plasmids are then cotransfected into insect cells or larvae with the transplacement plasmid and wild type CuniNPV, thus allowing the allelic replacement of the non-essential gene of CuniNPV with the desired promoter/insect-antagonistic gene construct. The desired recombinant CuniNPV is isolated after selection on the basis of its non-essential gene function-negative phenotype and screening for the proper allelic replacement events by restriction endonuclease analysis and Southern hybridization. (Miller et al. (1987) "Biotechnology in Invertebrate Pathology and Cell Culture" pp. 295–303; Miller et al. (1986) in Genetic Engineering. Principles and Methods, Vol. 8, eds. J. Setlow and A. Hollaender, Plenum Press, New York, pp.277–298; U.S. Pat. No. 5,266,317).

The present invention also provides methods for controlling baculovirus infections in invertebrates such as beneficial insects and members of the Crustacea, e.g. shrimp species such as *Penaeus duorarum* and *Penaeus aztecus*. The baculovirus known as "Baculovirus penaei", commonly known as "BP" and designated as PvSNPV (Francki, R. I. B., Fauquet, C. M., Knudson, D. L. and Brown, F. (Eds.) 1991 "Classification and Nomenclature of Viruses," 5th Report of the International Committee on Taxonomy of Viruses; Springer-Verlag, New York) is known to infect at least 14 species of penaeid shrimp and can cause serious epizootics with high mortality of larval and postlarval stages in some of those species (Lightner, D V and Redman R M 1991 Host, geographic range and diagnosis procedures for the penaeid virus diseases of concern to shrimp culturists in

the Americas; In "Frontiers in Shrimp research"; P. Deloach, W. J. Dougherty, and M. A. Davidson. eds., pp. 177–196; Elsevier, Amsterdam). BP is responsible for annual economic losses in cultured penaeid shrimp in the Americas and Hawaii due to mass mortalities that occur in the hatchery phase of production (Stuck, K C and Overstreet R M 1994 J Invertebr. Pathol 64:18–25). BP also commonly infects a substantial number of wild brown shrimp, *P. aztecus*, from the northern Gulf of Mexico (Overstreet, R M 1994 "BP in Penaeid Shrimps" In USMSFP 10th Anniversary Review, Gulf Coast Research Laboratory Special Publ. No. 1:97–106). The method disclosed herein comprises administering to the invertebrate an amount of calcium, iron or copper ions that is effective in reducing or eliminating baculoviral infections. In specific embodiments, the effective calcium, iron or copper ion concentration is 1 mM, 5 mM or 10 mM. In a specific embodiment, calcium, iron or copper ions are added to the water in which shrimp are living or being farmed to give an effective concentration of at least 1 mM.

The invention also provides an isolated nucleic acid comprising the nucleotide sequence set forth in SEQ ID NO:1; SEQ ID NO:4; SEQ ID NO:10; SEQ ID NO:19; SEQ ID NO:38; SEQ ID NO:42; SEQ ID NO:44; SEQ ID NO:46; SEQ ID NO:48; SEQ ID NO:50; SEQ ID NO:53; SEQ ID NO:61; SEQ ID NO:66; SEQ ID NO:70; SEQ ID NO:72; SEQ ID NO:74; SEQ ID NO:76; SEQ ID NO:80; SEQ ID NO:83; SEQ ID NO:87; SEQ ID NO:94; SEQ ID NO:106; SEQ ID NO:117; SEQ ID NO:130; SEQ ID NO:145, and SEQ ID NO:146, as well as allelic variants, homologs or unique fragments thereof. To be unique, the fragment must be of sufficient size to distinguish it from other known nucleic acid sequences, most readily determined by comparing any nucleic acid fragment to the nucleotide sequences of nucleic acids in computer databases of such sequences, such as GenBank. Such comparative searches are standard in the art. The fragment may code for a polypeptide, e.g. SEQ ID NO:147 or SEQ ID NO:148, or it may be a primer or probe sequence. Typically, a unique fragment useful as a primer or probe will be at least about 20 to about 25 nucleotides in length, depending upon the specific nucleotide content of the sequence. Additionally, fragments can be, for example, at least about 30, 40, 50, 75, 100, 200 or 500 nucleotides in length. The nucleic acids can be single or double stranded, and can be DNA or RNA, depending upon the purpose for which it is intended.

The present invention additionally provides an isolated nucleic acid that hybridizes under stringent conditions with a nucleic acid selected from the group of sequences set forth in SEQ ID NO:1; SEQ ID NO:4; SEQ ID NO:10; SEQ ID NO:19; SEQ ID NO:38; SEQ ID NO:42; SEQ ID NO:44; SEQ ID NO:46; SEQ ID NO:48; SEQ ID NO:50; SEQ ID NO:53; SEQ ID NO:61; SEQ ID NO:66; SEQ ID NO:70; SEQ ID NO:72; SEQ ID NO:74; SEQ ID NO:76; SEQ ID NO:80; SEQ ID NO:83; SEQ ID NO:87; SEQ ID NO:94; SEQ ID NO:106; SEQ ID NO:117; SEQ ID NO:130; SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, and SEQ ID NO:148. In a specific embodiment, stringent conditions would include an aqueous hybridization solution comprising the nucleic acid probe and 0.07 M NaH₂PO₄, 0.18 M Na₂HPO₄, 0.001 M EDTA, 7% SDS, 1% BSA at 65° C., followed by posthybridization washes as follows: 2xSSC/0.1%SDS at room temperature for 5 minutes, followed by two washes in 0.1xSSC/0.1%SDS at 65° C. for 20 minutes each. Such hybridizing nucleic acids can be fragments of the complementary strands for the referenced sequences or can be primers or probes that can identify the referenced sequences.

In a specific embodiment, the invention provides an isolated nucleic acid encoding a polypeptide comprising the amino acid sequence set forth in SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:30, or SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:75, SEQ ID NO:77, SEQ ID NO:79, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:10, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, or SEQ ID NO:144. Homologies of these amino acid sequences to sequences in the computer databases are presented in Tables 11 and 12. Table 11 presents a comparison of these CuniNPV amino acid sequences with known Lepidopteran baculovirus amino acid sequences. Table 12 presents non-baculoviral sequence matches to the CuniNPV amino acid sequences in the databases. The analyses presented in both tables were done using BLASTP 2.0.8 (Altschul, S F et al 1997 Nucleic Acids Res. 25:3389-3402).

The present invention additionally provides a purified polypeptide or protein encoded by a nucleic acid of this invention. Purified means substantially free from the naturally occurring materials with which the polynucleotide or polypeptide is normally associated in nature. The purified protein need not be homogeneous, but must be sufficiently free of contaminants to be useful in research or commercial applications, for example, for use in detecting or preparing antibodies to the protein, or in screening libraries of molecules for those molecules that interact with the protein. Greater levels of purity can be obtained using methods derived from well known protocols. The polypeptide or protein can be readily obtained by any of several means. For example, the nucleotide sequence encoding the polypeptide can be translated and then the corresponding polypeptide, or any portion thereof, can be synthesized mechanically by standard methods. Additionally, the nucleic acids encoding the polypeptide can be expressed or synthesized, an antibody specific for the resulting polypeptide can be raised by standard methods (see, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y. 1988), and the polypeptide can be isolated from infected mosquito larvae or cells by selective binding with the antibody. Such polypeptides can be purified

to the extent desired by standard methods of protein purification (see, e.g., Sambrook et al., *Molecular Cloning: A Laboratory Manual*, 2nd Ed., Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y., 1989). The antibodies so produced can be used as diagnostic tools for the presence of the virus.

As will be appreciated by those skilled in the art, the invention also includes those polypeptides having slight variations in amino acid sequences or other properties. Amino acid substitutions can be selected by known parameters to be neutral (see, e.g., Robinson W E Jr. and Mitchell W M., AIDS 4:S151-S162(1990)). Such variations may arise naturally as allelic variations (e.g., due to genetic polymorphism) or may be produced by human intervention (e.g., by mutagenesis of cloned DNA sequences). Such as induced point, deletion, insertion and substitution mutants. Minor changes in amino acid sequence are generally preferred, such as conservative amino acid replacements, small internal deletions or insertions, and additions or deletions at the ends of the molecules. Substitutions may be designed based on, for example, the model of Dayhoff, el al. (in *Atlas of Protein Sequence and Structure* 1978, Nat'l Biomed. Res. Found., Washington, D.C.). These modifications can result in changes in the amino acid sequence, provide silent mutations, modify a restriction site, or provide other specific mutations. Likewise, such amino acid changes result in a different nucleic acid encoding the polypeptides and proteins. Thus, alternative nucleic acids are also contemplated by such modifications.

The present invention also provides cells containing a nucleic acid of the invention. A cell containing a nucleic acid encoding a polypeptide typically can replicate the DNA and, further, typically can express the encoded polypeptide. The cell can be a prokaryotic cell, particularly for the purpose of producing quantities of the nucleic acid, or a eukaryotic cell, particularly an insect cell. The cell is preferably an insect cell for the purpose of expressing the encoded polypeptide so that the resultant produced polypeptide has insect cell-determined protein processing modifications.

Throughout this application, various publications are referenced. The disclosures of these publications in their entireties are hereby incorporated by reference into this application in order to more fully describe the state of the art to which this invention pertains.

EXAMPLES

Example 1

Methods

A. Field Collections

Mosquito larvae were collected from a man-made settling pond of swine effluent located in Gainesville, Fla. The pond was approximately 30 square meters and surrounded by elderberry trees (*Sambucus canadensis*) with pennywort (*Hydrocotyl ranunculoides*) and duckweed (*Lemna* spp.) along the margins. Samples were collected once or twice a week during the peak mosquito breeding periods and at least once a month during the off season.

Larvae were concentrated at the field site by straining 50–60 liters of field water through 60 mesh sieves at the site and placing the collected larvae in 15–30 liters of field water. In the laboratory, larvae were again strained through a series of 10, 18, 35 and 80 mesh sieves (2.0, 1.0, 0.5, 0.13 mm openings respectively) and the contents of each sieve washed into 300–800 ml of water. Third and fourth instar larvae were retained by the 35 and 18 mesh sieves while the first and second instar larvae were found in the 80 mesh

sieve. The total volume of water and larvae was measured from the 18 and 35 mesh sieves and after agitation, a sample of 10 to 100 ml removed, measured and the number of larvae counted. Larvae from the sample were examined for signs of infection and for species identification. The total number of larvae, the proportion of each species and the percentage infection was estimated from the samples of the two sieves. If a significant number of larvae were retained in the 10 mesh sieve, a sample was taken from it and included in the estimates. The estimate of the total number of larvae collected from the 35 mesh or larger was used as an indicator of the larval population.

B. Water Analysis and Characterization

Samples of the field water were prepared for chemical analysis by several methods. Water strained through 400 mesh (38 micron openings) was centrifuged at 4,800 g for 10 min and the supernatant frozen. In addition, 10 ml samples of the supernatant and unfiltered water were digested in 1 N HNO₃ by heating a 1:1 mixture of water: 1 N HNO₃ to just below the boiling point until the volume had been reduced to 1–2 ml. The residue was reconstituted in 1 N HNO₃ and held at room temperature. In addition, unfiltered water was filtered through a Whatman No. 41 filter and stored frozen. Water samples were submitted for elemental analysis to the University of Florida Analytical Research Laboratory (Room 631 Wallace Building, University of Florida, Gainesville, Fla.). Cation concentrations were obtained using ICAP argon plasma (Thermo-Jerrell-Ash Corp, 27 East Forge Parkway, Franklin, Mass. 02038). The conductivity of the field water was 1.8±0.4 mmhos and the pH averaged 7.8±0.03 (n=92). A sample of field water was analyzed to determine the content of 20 cations. Potassium, sodium, magnesium, and calcium accounted for 90% of the cations with potassium having the highest concentration. Additional water samples were evaluated for these predominant cations, and the average concentrations are summarized in Table 4.

C. Electron Microscopy

Infected larvae were prepared for ultrastructural examination by fixing dissected guts in 2.5% glutaraldehyde for 2 hr, postfixing in 2% osmium tetroxide, dehydrating in ethanol series and embedding in epon-araldite. Thin sections, stained in uranyl acetate and lead citrate, were photographed at 75 kV. Suspensions of virions, released by alkaline treatment, were negatively stained in 1% PTA on coated grids and photographed at 75 kV.

D. Laboratory Bioassay

Groups of 100 *Culex quinquefasciatus* larvae, 3 or 4 days old, were exposed in 4 oz plastic cups in 100 ml of water with 2 ml of 2% alfalfa and potbelly pig chow mixture (2:1). In paired tests, virus from eight infected larvae were homogenized and added to the field water while the other cup had no virus added. Larvae were exposed in one of the following: field water strained through 400 mesh sieves, field water supernatant, field water pellet, or deionized water. Different salt mixtures were made up, each one using all but one of the following: 1.8 mM MgCl₂, 0.5 mM CaCl₂, 6.0 mM KCl, 1.8 mM NaCl and 3 mM NH₄Cl. Additionally, in paired tests, larvae were exposed in containers with and without the addition of 10 mM MgCl₂, and with and without virus. Additional treatments included alkali pretreatment of the virus prior to exposure (Federici B A and Lowe, 1972 *J. Invertebr. Pathol.* 20:14–21) and the addition of the optical

brightener Calcofluor M2R (Shapiro and Robertson, 1990, *J. Econ. Entomol.* 85: 1120–1124). After 48 hrs, the larvae were removed and examined for signs of infection. Only those larvae with hypertrophied nuclei either in the midgut or the gastric caecae were scored as positive.

E. Isolation of CuniNPV and Molecular Characterization

Density gradient centrifugation of homogenized infected larvae on a continuous Ludox HS40 gradient (DuPont), commonly used to isolate microsporidia, was adapted to efficiently purify occlusion bodies (Undeen, A H and J V avra, 1997, Research methods for entomopathogenic Protozoa, In: Manual of Techniques in Insect Pathology, L. A. Lacey (Ed.), 117–151, San Diego: Academic Press). After centrifugation was completed, the band containing the inclusion bodies was washed in 0.001N NaOH, pH 10.0 to efficiently remove all of the silica. Washing only in deionized water leaves traces of silica that can crystallize and interfere with later manipulations of the inclusion bodies.

10 DNA was extracted using standard protocols. Pulsed field gel electrophoresis and restriction digests with Eco RI, BamHI, and PstI were conducted to determine the genome size.

F. Sequencing of CuniNPV

Viral DNA with digested with a restriction enzyme (HindIII, PstI, or EcoRI), and the fragments were cloned into pUC19 (shotgun cloning). To clone larger fragments, digested viral DNA was electrophoresed, and the band(s) of interest were eluted from the gel. Sequencing of purified

30 fragments was done at the University of FLorida DNA Sequencing Core Laboratory (Gainesville, Fla.) using the Taq DyeDeoxy Terminator protocols developed by Applied Biosystems (Perkin-Elmer Corp., Foster City, Calif.) and fluorescence-labeled dideoxynucleotides and primers. Oligo primers were designed using OLIGO 4.0 (National BioSciences, Inc., Plymouth, Minn.) and synthesized at the DNA Synthesis Core Laboratory (University of FLorida, Gainesville, Fla.). The labeled extension products were

35 analyzed on an Applied BioSystems Model 373A or 377 DNA sequencer Perkin Elmer Corp., Foster City. Calif.). Nucleotide sequences were aligned and assembled using programs in the Sequencher 3.0 software package (Gene Codes Corp., An Arbor, Minn.).

G. Mosquito Susceptibility to CuniNPV

CuniNPV produced in *Culex quinquefasciatus* and purified on a Ludox HS40 continuous gradient was used for all tests. Mosquito larvae of various species were obtained from

50 laboratory-reared stock or from field isolations. Larvae were 48 hours old at the time of the bioassays. Groups of 100 healthy larvae were counted into cups with 100 ml of 10 mM MgCl₂.

55 For each test, one group was exposed to 10 larval equivalents of CuniNPV and one group was not exposed to the virus, thus serving as a control. To test the susceptibility

of the predacious mosquito, *Toxorhynchites ambionensis*, 20 second instar larvae were set up individually in well plates with 10 mM MgCl₂ and fed 3 live *Cx. quinquefasciatus*

60 larvae infected with NPV. Similar groups of *Tx. ambionensis* were fed healthy *Cx. quinquefasciatus* larvae and served as a control. One hundred healthy *Cx. quinquefasciatus* larvae, exposed at the same time as the test species, served as positive controls to verify the infectivity of the virus being tested. After 48 hours, all larvae were examined for presence of infection and mortality was calculated. In tests where the

positive control gave infection levels lower than 80%, the data was discarded.

Example 2

Host Range of the NPV

Collections of *Cx. nigripalpus* made at different times during the year showed that the presence of four species of Culex varies over the year. *Culex nigripalpus* were present during the warmer months while *Culex quinquefasciatus* were present in cooler months and during the winter. *Culex salinarius* and *Culex restuans* were also present during the winter. A few *Anopheles crucians* were found in the summer and *Culiseta inornata* were present occasionally in the cooler months.

Table 1 compares the CuniNPV infection rate in the four Culex species collected. *Culex nigripalpus* was the most common mosquito and infected larvae were present in 90% of the collections. The average infection rate was $20.1 \pm 2.3\%$ with a maximum rate of 60%. The next most frequently collected mosquito was *Cx. quinquefasciatus*, which was present in 49% of the collections. The average infection rate was $7.8 \pm 2.0\%$ and the maximum infection rate was 20%. Infected *Cx. salinarius* were present in 34% of the collections with an average infection rate of $11.5 \pm 4.6\%$ and a maximum rate of 30%. *Culex restuans* were present in 6% of the collections and no CuniNPV infected *Cx. restuans* were observed.

Larvae infected with a cytoplasmic polyhedrosis virus were collected in January through March in 1997 and 1998. *Culex restuans*, *Cx. quinquefasciatus*, and *Cx. salinarius* were all infected with the CPV. The highest CPV infection rate was 18%. *Culex nigripalpus* was not present during this time period.

During September to October 1996, the population of *Cx. nigripalpus* was extremely high with collections of 4,300 to 42,000 larvae and the NPV infection rate was as high as 31%. The populations of Culex species fluctuates throughout the year. During March through December 1997, the largest collection was 24,000 larvae consisting of *Cx. salinarius* and *Cx. restuans*. *Culex nigripalpus* was the predominant mosquito by June through October 1997. For an eight week period from July to September 1997, NPV infected larvae were found in all of the species collections. Table 2 compares the average number of larvae collected and the percentage infection rate for two epizootic periods in 1996 and 1997. In 1997, the population was significantly reduced and the percentage of CuniNPV infected larvae was higher than the 1996 period.

Example 3

Laboratory Transmission

Colony *Cx. quinquefasciatus* were infected when exposed in field water at a rate ranging from 6–20%, but when insects were exposed in deionized water, the infection rate dropped to between 0 and 3%. Alkali pretreatment and the use of optical brighteners were ineffective in increasing the infection rate in deionized water. Table 3 compares the infection rates from the field samples and assays with colony *Cx. quinquefasciatus* in field water with and without virus.

Statistical comparison by a student t-test shows that the difference between infection rates in field water with (35.4% ave.) or without virus (10.7% ave) is significant. In contrast, the infection rate of the virus in deionized water averaged less than 1%. These experiments demonstrate that there is/are additional factor/activator(s) present in the field water that is/are necessary to obtain higher rates of infection of larvae by the virus.

To identify such factors, a correlation analysis between the percentage infection in colony mosquitoes exposed to different samples of field water to which virus is added, and the four cations individually, expressed either as a concentration or as a percentage of the total cation content in the field water is presented in Table 4. There is a negative correlation between the percentage infection and either total water conductivity, K, Na or Ca, while there is a positive correlation with Mg. Alternatively, when the infection percentage is correlated with each cation expressed as a percentage of the principle cations (e.g. Mg/(K+Na+Mg+Ca)), only Mg has a significant correlation.

Table 5 summarizes the results from the bioassay of larvae exposed to virus in salt mixtures. Compared to the negative results routinely obtained with deionized water, the addition of a salt mixture significantly improves the infectivity of the virus (which can also be termed the susceptibility of larvae). Further analysis shows that the only salt that enhanced infectivity on its own is MgSO₄, while the infectivity in a salt mixture that does not include CaCl₂ was more than doubled. These Ca⁺⁺-lacking mixtures, which contain 1.8 mM Mg⁺⁺, have some infectivity, while there is no infectivity in mixtures without any Mg⁺⁺.

Results of infectivity studies using other divalent cations show that several other cations are potential activators, while a few inhibit infection. Table 6 presents data on additional cations, including barium, cobalt, nickel and strontium, which significantly improve the infectivity of the virus. Table 7 demonstrates that copper and iron, in addition to calcium, inhibit infection when added with Mg⁺⁺. Manganese was neutral in its effect. Tin and zinc were too toxic to determine their effect on infectivity.

Example 5

Mosquito Host Range and Morphology of Infection

A. Mosquito Host Range

The CuniNPV infected only species of Culex including *Cx. nigripalpus*, *Cx. quinquefasciatus* and *Cx. salinarius* (Table 8). The only other Culex species tested, *Cx. restuans*, was not susceptible using laboratory-reared insects.

B. Symptomatology

Gross morphology. Larvae of *Cx. quinquefasciatus* and *Cx. nigripalpus* exposed to CuniNPV are typically stunted in development when compared to unexposed individuals. The first signs of infection are observed 24–28 hours post-exposure in cells of the gastric caecae and posterior midgut epithelium. The nuclei of the infected cells are hypertrophied and appeared opaque to white in color due to the proliferation of occlusion bodies within the nuclei. Nuclei of cells in the anterior midgut are rarely infected. Within 48 hours post-exposure many infected nuclei of the gastric caecae and posterior midgut are filled with occlusion bodies. Death of the larvae usually occurs within 72–96 hours.

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Fine Morphology. Occlusion bodies of CuniNPV are restricted to nuclei of the midgut epithelium and gastric caecae. Occlusion bodies are globular in shape with a diameter of approximately 300 nm, and they do not have a membrane surrounding them, as is typical for other baculoviruses. Each occlusion body contains up to about 8 rod-shaped virions. The rod-shaped virions were approximately 200×40 nm and composed of a nucleocapsid, intermediate layer and an outer envelope.

Example 6**Biochemical/Molecular Characterization of CuniNPV**

The occlusion bodies have a density of 1.14–1.18 g/ml and are sensitive to agglutination upon freezing. Based on pulse field gel electrophoresis and restriction digests with Eco RI, BamHI, and PstI, the genome size of CuniNPV is approximately 70–75 kb. Sequences obtained from a CuniNPV were analyzed for the presence of open reading frames (orf), i.e. sequences coding for polypeptides, and the identified orfs were compared to known sequences in publicly available computer databases to identify homologies. Table 11 presents homologies between the novel orfs from the mosquito-infecting baculoviruses of this invention and known polypeptides from Lepidopteran baculoviruses. Table 12 presents the “best matches”, i.e. the highest homologies, between the novel orfs from the mosquito-infecting baculoviruses of this invention and known polypeptides in the database.

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30**20**

mosquitoes are ground into a powder, and MgCl₂ is mixed into the powder, in an amount sufficient to promote infection. If additional inert carrier is needed, corn cob grits can be added.

Another formulation involves the preparation of a microencapsulated baculovirus preparation using lignin and magnesium, according to methods described in U.S. Pat. No. 5,750,467. The following formulations were tested:

Formulation 1: 6 g lignin, 0.6 g Mg carbonate, 0.066 g virus

Formulation 2: 6 g lignin, 0.06 g Mg, 0.066 g virus

Formulation 3: 6 g lignin, 6 g Mg, 0.6 g Ca, 0.072 g virus

Formulation 4: 6 g lignin, 6 g Mg, 0.6 g Ca, 0.126 g virus

Formulation 5: 6 g lignin, 0.6 g Mg, 0.066 g virus

Formulation 6: 6 g lignin, 0.06 g Mg, 0.06 g. virus

Example 9**Improved Transmission of AesoNPV**

A mosquito baculovirus originally isolated in Louisiana from *Aedes sollicitans* (AesoNPV) was tested against a variety of mosquitoes. As shown in Tables 9 and 10, MgCl₂ enhances infectivity approximately 4-fold for *Aedes triseriatus*. In tests with *Aedes aegypti*, usually a poor host for this virus, a 7-fold increase in infectivity was obtained. Also, it was possible to infect a *Culex* species with a baculovirus from an *Aedes* host for the first time by using Mg⁺⁺.

TABLE 1

Average infection rate of *Culex* spp. from collections during October 1996 through January 1998 (79 total collections).

	<i>Cx. nigripalpus</i>	<i>Cx. quinquefasciatus</i>	<i>Cx. salinarius</i>	<i>Cx. restuans</i>
Present	10/96–1/97 4/97–12/97 45	10/96–5/97 9/97–1/98 11	1/97–3/97 1/98 8	1/97–3/97 1/98 0
No. collections with infected larvae in sample				
No. collections with specified species in samples	71	39	27	5
Average percentage infection (positive collections only)	20.1 ± 2.3	7.8 ± 2.0	11.5 ± 4.6	0
Max infection rate	60	20	30	0
Average field infection rate (positive only)	15.6 ± 1.9	9.9 ± 2.4	9.3 ± 1.3	7.7 ± 1.9

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Example 7**Production of CuniNPV**

2500 3-day old *Culex nigripalpus* or *Cx. quinquefasciatus* larvae are exposed to 100 larval equivalents of CuniNPV in 3 liters of 14 mM MgSO₄. This yields 100% infection, and Virus is harvested at 48 hour post-exposure. Large numbers of trays can be produced quickly to provide large amounts of virus.

Example 8

Formulations for Insecticidal Compositions
Compositions suitable for applying to mosquito habitats can be made from air-dried, infected mosquitoes. The dried

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TABLE 2

Comparison of two epizootic periods of nuclear polyhedrosis virus in *Culex nigripalpus*.

	Culex Population Index	NPV Infection Rate
8/28/96–10/21/96 (N = 8)		
Average ± SE Minimum	15,000 ± 4,300 4,300	10.6 ± 3.7% 1.4%

65

TABLE 2-continued

Comparison of two epizootic periods of nuclear polyhedrosis virus in *Culex nigripalpus*.

	Culex Population Index	NPV Infection Rate
Maximum	42,000	31.1%
7/10/97-9/2/97 (N = 8)		
Average \pm SE	4,000 \pm 1,000	28.9 \pm 4.6%
Minimum	1,700	11.6%
Maximum	9,700	48.0%

TABLE 5

Percentage infection in colony *Culex quinquefasciatus* in salt mixtures of 6.0 mM KCl, 1.8 mM NaCl, 0.5 mM CaCl₂ and 1.8 mM MgCl₂. % Infection

Media	Salt Mixture without Component		Component Alone
	10	13.6%	
Complete Salt Mixture	13.6%		
CaCl ₂	19.9%		0.0%
MgCl ₂ or MgSO ₄	0.0%		10.9%
KCl	8.6%		0.0%
NaCl	3.0%		0.0%

TABLE 3

Infection rate of Culex spp. collected in the field and colony *Culex quinquefasciatus* exposed in field water with and without virus added.

Field	Colony <i>Culex quinquefasciatus</i>				
	Infection Rate of Culex spp.	Field Water	Field Water + Virus	Dionized Water + Virus	10 mM MgCl ₂
N	61	61	57	22	68
Average \pm SE	10.7 \pm 1.7%	8.9 \pm 1.6%	35.4 \pm 3.1%	0.5 \pm 0.2%	68.1 \pm 3.5%
Maximum Paired Differences	48.0%	50.0%	94.8%	3.0%	100%
Assay in Field Water-Field Infection Rate Assays in Field Water plus virus-Field Water		-1.5 \pm 1.2%			
		25.8 \pm 2.9% ^A			

*Not significantly different from zero.

^ASignificantly different from zero.

TABLE 4

Concentration of principle cations and the correlation coefficient and probability of $> |R|$ of percentage infection with cation content of field water and the conductivity of the samples.

Mean \pm SE N = 22	Concentration (mM)				
	R	% of Principle Cations			
	(sign from slope)	Prob > R	R (sign from slope)	Prob > R	
K	10.7 \pm 0.5	-0.28	0.19	-0.37	0.10
Na	3.2 \pm 0.2	-0.31	0.18	-0.37	0.10
Mg	1.9 \pm 0.1	0.01	0.96	0.46	0.03
Ca	0.8 \pm 0.05	-0.15	0.52	0.1	0.68
Conductivity (mmhos)	2.0 \pm .06	-0.33	0.14		

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TABLE 5-continued

Percentage infection in colony *Culex quinquefasciatus* in salt mixtures of 6.0 mM KCl, 1.8 mM NaCl, 0.5 mM CaCl₂ and 1.8 mM MgCl₂. % Infection

Media	Salt Mixture without Component		Component Alone
	50	0.0%	
Deionized Water		0.0%	

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TABLE 6

Activation potential of cations tested with NPV against *Culex quinquefasciatus*. Activation by Various Cations Activators:

Cation	Dose Range (mM)	% Infection Range
Ba	1.25-10.0	5.5-12.5
Co	0.1-0.63	17.3-35.9
Mg	2.0-40.0	18.1-100.0
Ni	0.05-0.2	11.3-95.5

60

65

TABLE 6-continued

Activation potential of cations tested with NPV against <i>Culex quinquefasciatus</i> .		
Activation by Various Cations		
Activators:		
Cation	Dose Range (mM)	% Infection Range
Sr	1.25–10.0	8.5–81.4
Ca	Inhibitor	
Cu	Inhibitor	
Fe	Inhibitor	
Mn	not	
Sn	maybe	
Zn	maybe	

TABLE 7

Different mosquito species exposed to 3–5 larval equivalents of NPV from <i>Aedes sollicitans</i> in the presence of MgCl ₂			
Species Tested	N	% Mortality*	% Infection
<i>Ae. triseriatus</i>	900	12.1	77.3
<i>Ur. iowii</i>	55	5.6	77.0
<i>Cx. nigripalpus</i>	200	27.7	38.0
<i>Ae. aegypti</i>	500	9.3	26.9
<i>Ae. albopictus</i>	100	3.1	—
<i>Ae. taeniorhynchus</i>	100	—	—
<i>Cx. quinquefasciatus</i>	100	—	—

20 *Abbott corrected

TABLE 8

Results of NPV Bioassays against mosquito larvae				Magnesium Dose Response Test				
Mosquito Species Tested	Number of Tests	% Mortality*	% Infection	Mosquito Species	[MgCl ₂] mM	Viral Dosage (LE)	% Mortality	% Infection
<i>Aedes aegypti</i>	4	0	0	<i>Ae. triseriatus</i>	100	10	0	26
<i>A. albopictus</i>	3	0	0	<i>Ae. triseriatus</i>	100	2.5	5	27
<i>A. triseriatus</i>	3	0	0	<i>Ae. triseriatus</i>	100	5	5	100.0
<i>A. taeniorhynchus</i>	3	0	0	<i>Ae. triseriatus</i>	100	10	5	19
<i>Anopheles albimanus</i>	4	7.9 ± 1.4	0	<i>Ae. triseriatus</i>	100	0	5	21
<i>A. quadramaculatus</i>	4	0	0	<i>Ae. triseriatus</i>	100	10	0	98
<i>Culex nigripalpus**</i>	2	9.0 ± 1.0	42.9 ± 7.1	<i>Ae. aegypti</i>	100	10	5	—
<i>C. quinquefasciatus</i>	7	5.0 ± 1.7	88.2 ± 2.9	<i>Ae. aegypti</i>	100	10	0	81
<i>C. restuans**</i>	1	2.1	0	<i>Ae. aegypti</i>	100	10	5	28.4
<i>C. salinarius**</i>	2	0	32.9 ± 9.8	<i>Ae. aegypti</i>	100	10	5	93
<i>Culexita melanura</i>	2	0	0	<i>Ae. aegypti</i>	100	0	5	4.3
<i>Toxorynchites ambionensis</i>	1	0	0					

*Abbot-corrected Mortality

**Egg rafts collected from the field and reared in the laboratory

TABLE 11

SEQ ID NO	Full Length (nt)	Position (length, ORF a)	Homology to Lepidopteran Baculovirus Amino Acid Sequences (length, aa)	AA Identities	AA Positives	E Value
10	6621	1	LdNPV LEF-1 (234) (235)	48/197 (24%)	80/197 (40%)	1e-08
			BmNPV LEF-1 (270)	52/200 (26%)	83/200 (41%)	4e-08
			CfNPV LEF-1 (251)	56/202 (27%)	82/202 (39%)	2e-07
			OpNPV LEF-1 (243)	54/200 (27%)	80/200 (40%)	3e-07
			AcNPV LEF-1 (266)	51/200 (25%)	81/200 (40%)	6e-07
			CINPV LEF-1 (246)	52/203 (25%)	79/203 (38%)	4e-06
10	6621	2	AcNPV 1 23.0 kd protein in HE65-PK2 intergenic region (204) (203)	65/200 (32%)	107/200 (53%)	1e-26
			OpNPV hypothetical 22.1 kd protein (orf115) (205)	66/204 (32%)	106/204 (51%)	2e-26
			BmNPV-AcMNPV orf115 (204)	64/203 (31%)	105/203 (51%)	4e-26
			LdNPV unknown (203)	55/156 (35%)	86/156 (54%)	3e-25
			XnGV-AcNPV orf115 homolog (61)	18/54 (33%)	30/54 (55%)	0.001
			LdNPV unknown (530)	51/215 (23%)	78/215 (35%)	1.1
44	1018	1	OpNPV ODV-E56 (374) (294)	90/253 (35%)	133/253 (51%)	8e-26
			CfNPV ODV-E56 (37)	88/248 (35%)	126/248 (50%)	1e-25
			LdNPV envelope protein (356)	94/290 (32%)	145/290 (49%)	3e-25
			CpGV ODV-E56 (355)	85/279 (30%)	144/279 (51%)	9e-25
			AcNPV ODV-E56 (376)	76/249 (30%)	124/249 (49%)	1e-21
			BmNPV ODV-E56 (= AcNPV orf148) (375)	73/251 (29%)	127/251 (50%)	1e-20
			HzNPV ODV-E56 (= AcNPV orf148 homolog) (175)	59/168 (35%)	88/168 (52%)	2e-18
			XnGV envelope protein homolog (190)	35/129 (27%)	63/129 (48%)	6e-05

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TABLE 11-continued

SEQ ID NO	Full Length (nt)	Position (length, ORF a)	Homology to Lepidopteran Baculovirus Amino Acid Sequences (length, aa)	AA Identities	AA Positives	E Value
66	2227	1 222-1256 (344)	LdNPV envelope protein p74 (672) CfNPV p74 protein (645) OpNPV p74 protein (644) AcNPV p74 protein (645) SiNPV (<i>Spodoptera littoralis</i>) p74 protein (657) BmNPV p74 (= AcNPV orf138) (645) SiNPV (<i>S. littoralis</i>) p74 protein (657) LsNPV p74 (366) BsNPV unknown protein (196) LdNPV unknown protein (390)	101/318 (31%) 76/212 (35%) 75/212 (35%) 78/248 (31%) 90/307 (29%) 73/208 (35%) 72/210 (34%) 68/204 (33%) 53/190 (27%) 44/165 (26%)	166/318 (51%) 121/212 (56%) 121/212 (56%) 133/248 (53%) 160/307 (51%) 119/208 (57%) 122/210 (57%) 120/204 (58%) 93/190 (48%) 71/165 (42%)	3e-38 8e-35 8e-35 3e-34 4e-34 6e-34 3e-32 1e-30 3e-12 0.007
66	2227	2 1195-2226 (343)	OpNPV LEF-4 (457)	25/88 (28%)	37/88 (41%)	0.37
72	827	1 256-696 (146)				
83	3198	1 2-2782 (926)	MbNPV DNA polymerase (628) SiNPV (<i>S. littoralis</i>) DNA polymenase (603) HzNPV DNA-directed DNA polymerase (1020) SeNPV DNA polymerase (636) HaNPV DNA polymerase (623) LdNPV DNA polymerase (1014) XnGV DNA polymerase (1098) AcNPV DNA polymerase (984) BsNPV DNA polymerase (674) LdNPV DNA polymerase (1013) BmNPV DNA polymerase (988) OaNPV DNA polymerase (658) OpNPV DNA polymerase (985) CfNPV DNA polymerase (990)	152/607 (25%) 166/662 (25%) 175/709 (24%) 151/608 (24%) 155/604 (25%) 146/622 (23%) 207/873 (23%) 185/788 (23%) 169/624 (27%) 149/615 (24%) 181/759 (23%) 151/627 (24%) 171/782 (21%) 170/779 (21%)	274/607 (45%) 284/662 (42%) 309/709 (42%) 267/608 (43%) 269/604 (43%) 269/622 (42%) 361/873 (40%) 339/788 (42%) 282/624 (45%) 269/615 (43%) 325/759 (41%) 262/627 (41%) 310/782 (38%) 306/779 (38%)	3e-45 8e-44 4e-41 5e-41 1e-39 1e-39 1e-38 8e-38 1e-37 3e-37 7e-37 2e-30 6e-30 9e-28
94	6627	3 2122-3111 (329)	AcNPV viral capsid associated protein (42.1 kDa protein in LEF8-FP intergenic region) (365) BmNPV VP1054 = AcMNPV orf54 (365) LdNPV LdOrf-57 peptide (332)	73/294 (24%)	123/294 (41%)	2e-05
94	6627	7 5920-6516 (198)	OpNPV hypothetical 42.5 kDa protein (ORF58) (378) AcNPV 33 kd early protein homolog (P33), (259) BmNPV AcNPV orf92 (259) OpNPV 33 kd early protein (P33) (282) LdNPV unknown (251) XnGV AcNPV orf92 homolog (115)	22/78 (28%), 33/133 (24%) 31/133 (23%) 42/154 (27%) 43/171 (25%) 18/51 (35%)	41/78 (52%) 62/133 (45%) 62/133 (46%) 72/154 (46%) 67/171 (39%) 28/51 (54%)	0.034 3e-05 5e-05 3e-04 0.003 0.98
117	7212	2 4239-5351 (370)	AcNPV 33 kDa early protein homolog, AcORF-92 peptide (259) BmNPV AcMNPV orf92 (259) OpNPV 33 kDa early protein (282) LdOrf-92 peptide (251) XnGV AcNPV ORF92 homolog (115) LdNPV envelope protein (676)	36/140 (25%) 34/140 (24%) 45/161 (27%) 52/198 (26%) 21/58 (36%) 24/91 (26%)	65/140 (45%) 65/140 (46%) 75/161 (45%) 78/198 (39%) 32/58 (53%) 44/91 (47%)	3e-07 6e-07 4e-06 1e-05 0.013 1.3
117	7212	3 441-1430 (329)	AcNPV hypothetical 42.1 kd protein in LEF8-FP intergenic region (365) BmNPV VP1054 (= AcNPV orf54) (365) LdNPV LdOrf57 peptide (332) OpNPV hypothetical 42.5 kd protein (orf58) (378)	73/294 (24%)	123/294 (41%)	2e-05
				71/294 (24%) 58/224 (25%) 22/78 (28%)	124/294 (42%) 87/224 (37%) 41/78 (52%)	2e-05 0.003 0.034
				71/294 (24%) 58/224 (25%) 22/78 (28%)	124/294 (42%) 87/224 (37%) 41/78 (52%)	2e-05 0.003 0.034

TABLE 12

SEQ ID NO	Length (nt)	Position (length, ORF SEQ aa)	Best Match (length, aa)	aa Identities	aa Positive	E Value
1	2446	1 8-1399 (463)	Human papillomavirus type 12 early protein (494)	31/113 (27%)	46/113 (40%)	0.96
		2 1522-2250 (242)	Fowlpox virus hypothetical protein 8 (154)	19/74 (25%)	32/74 (42%)	1.8
		3 226-627 (133)	<i>Caenorhabditis elegans</i> predicted using gene finder (360)	22/79 (27%)	35/79 (43%)	0.43
		4 2-208 (68)	Putative transposase Y4UI, Rhizobium sp. transposase homologue (514)	20/54 (38%)	27/52 (%1%)	2.3
		5 1-195 (64)	<i>Pseudomonas stutzeri</i> polyhydroxybutyrate depolymerase (576)	14/41 (34%)	19/41 (46%)	6.7
		6 1954-2124 (56)	—	—	—	—
		7 963-1124 (53)	Chain A, structure of diferric mare lactoferrin at 2.62a resolution (689)	13/44 (29%)	21/44 (47%)	9.1
10	6621	1 2630-3337 (235)	LdNPV late expression factor (LEF) 1 (234)	48/197 (24%)	80/197 (40%)	1e-8
		2 1887-2498	AcNPV (orf 115), hypothetical 23.0 kd protein in HE65-PK2	56/155 (36%)	88/155 (56%)	1e-25

TABLE 12-continued

SEQ ID NO	Length (nt)	ORF SEQ aa	Position (length, aa)	Best Match (length, aa)	aa Identities	aa Positive	E Value
			(203)	intergenic region (204)			
3	4813-5388		(191)	<i>Saccharomyces cerevisiae</i> protein kinase 1 (1063)	16/48 (33%)	25/48 (51%)	1.7
4	11-544		(177)	<i>Coprinus cinereus</i> pheromone receptor (518)	15/51 (29%)	25/51 (48%)	2.7
5	3601-4125		(174)	human, peptide, T-cell receptor alpha chain, TCR alpha (TLC RB129) (129)	26/117 (22%)	50/117 (42%)	4.5
6	5333-5851		(172)	<i>Xenopus laevis</i> membrane anchored metalloprotease; disintegrin; cysteine-rich protein (706)	23/79 (29%)	37/79 (46%)	2.5
7	4076-4423		(118)	<i>Bacillus subtilis</i> methionyl-tRNA synthetase (664)	14/36 (38%)	17/36 (46%)	4.5
8	1278-1631		(117)	<i>Saccharomyces cerevisiae</i> probable membrane protein YPR049c-yeast(1178)	25/67 (37%)	34/67 (50%)	0.4
9	1444-1791		(115)	<i>Prunus dulcis</i> extensin (278)	13/33 (39%)	17/33 (51%)	1.4
10	534-860		(108)	<i>Dictyostelium discoideum</i> spore coat protein SP87 (677)	24/81 (29%)	33/81 (40%)	0.87
11	901-1224		(107)	Gallus gallus slow myosin heavy chain 2 (761)	20/67 (29%)	39/67 (57%)	0.042
12	3977-4288		(103)	mouse neural cell adhesion molecule long domain form precursor(1115)	20/64 (31%)	31/64 (48%)	3.2
13	5892-6191		(99)	Glycine max guanine nucleotide regulatory protein (211)	20/76 (26%)	27/76 (35%)	2.1
14	4458-4742		(94)	human glutamate decarboxylase (EC 4.1.1.15) (593)	21/55 (38%)	24/55 (43%)	5.3
15	1640-1885		(81)	—	—	—	—
16	2243-2476		(77)	envelope surface glycoprotein SU-feline leukemia virus (strain Sarma) (404)	17/59 (28%)	25/59 (41%)	5.9
17	6432-6623		(65)	Hepatitis G virus polyprotein (2842)	14/35 (40%)	18/35 (51%)	8.7
18	965-1156		(63)	<i>Lotus japonicus</i> rac GTPase activating protein 1 (493)	18/52 (34%)	23/52 (43%)	1.0
19	4404-4592		(62)	<i>Drosophila melanogaster</i> probable transcriptional regulator dre4 (1059)	16/56 (28%)	28/56 (49%)	1.3
20	3865-4044		(59)	—	—	—	—
21	1371-2541		(56)	<i>Saccharomyces cerevisiae</i> Sds3 protein-hypothetical (327)	12/25 (48%)	13/25 (52%)	6.9
22	2683-2835		(50)	<i>Oncorhynchus mykiss</i> retinoblastoma 1 (910)	12/40 (30%)	24/40 (60%)	3.1
38	1300	1	2-1299 (432)	<i>Methanococcus jannaschii</i> P115 homolog (1169)	78/349 (22%)	153/349 (43%)	7e-9
		2	539-919 (126)	<i>Escherichia coli</i> putative O-antigen transporter (415)	24/81 (29%)	39/81 (47%)	3.6
		3	858-1211 (117)	<i>Schizosaccharomyces pombe</i> hypothetical 41.0 kDa protein C1F8.06 in chromosome 1 (385)	28/89 (31%)	42/89 (46%)	1.3
44	1018	1	85-969 (294)	OpNPV occlusion derived virus envelope protein E56 (ODV-E56) (374)	70/199 (35%)	103/199 (51%)	7e-19
		2	133-336 (67)	Rhodococcus sp. transposase (754)	16/39 (41%)	23/39 (58%)	2.9
48	1076	1	1-1074 (357)	<i>Arabidopsis thaliana</i> , similar to Homo copine I (644)	33/144 (22%)	64/144 (43%)	2.1
		2	180-362 (60)	<i>Pyrococcus horikoshii</i> long hypothetical protein (102)	13/27 (48%)	18/27 (66%)	8.9
		3	1-153 (50)	<i>Danio rerio</i> LIM-domain binding factor 4; LDB4 (374)	15/41 (36%)	24/41 (57%)	4.1
53	1656	1	242-1528 (428)	<i>Klebsiella pneumoniae</i> citrate carrier protein (444)	157/411 (38%)	231/411 (56%)	8e-78
		2	434-1655 (407)	—	—	—	—
		3	867-1430 (187)	<i>Homo sapiens</i> KIAA0324 (1288)	47/187 (25%)	71/187 (37%)	0.19
		4	894-1187 (97)	<i>Drosophila melanogaster</i> hoemetic protein spalt-major (1355)	26/90 (28%)	38/90 (41%)	0.42
		5	1440-1655 (72)	Chilo iridescent virus putative small basic protein (57)	17/30 (56%)	20/30 (66%)	0.53
		6	1180-1341 (53)	<i>Streptomyces coelicolor</i> hypothetical protein in PRJL 5' region (ORF 1) (256)	19/47 (40%)	25/47 (52%)	1.1
		7	94-255 (53)	<i>Mycobacterium tuberculosis</i> hypothetical protein Rv1232c (435)	16/43 (37%)	20/43 (46%)	0.8
		8	64-219 (51)	<i>Mycobacterium tuberculosis</i> hypothetical 36.6 kDa protein CY338.11C precursor (1289)	18/47 (38%)	24/47 (50%)	1.8
66	2227	1	222-1256	LdNPV envelope protein p74 (672)	101/318 (31%)	166/318 (51%)	3e-38

TABLE 12-continued

SEQ ID NO	Length (nt)	ORF SEQ	Position (length, aa)	Best Match (length, aa)	aa Identities	aa Positive	E Value
		(344)					
		2 1195–2226	LdNPV unknown (390)	44/165 (26%)	71/165 (42%)	0.007	
		(343)	—	—	—	—	
		3 116–589	—	—	—	—	
		(157)					
72	827	1 256–696	OpNPV late expression factor 4 (LEF-4) (457)	25/88 (28%)	37/88 (41%)	0.38	
		(146)					
		2 264–614	<i>Toxoplasma gondii</i> micronemal protein MIC2 (769)	30/95 (31%)	41/95 (42%)	0.35	
		(116)					
76	692	1 27–691	—	—	—	—	
		(221)					
		2 324–691	—	—	—	—	
		(122)					
		3 3–164	—	—	—	—	
		(53)					
		4 13–168	—	—	—	—	
		(51)					
83	3198	1 1–2771	MbNPV DNA polymerase (628)	148/607 (24%)	270/607 (44%)	1e-40	
		(923)					
		2 2520–3208	<i>Bos taurus</i> beta-1 integrin subunit (773)	28/108 (25%)	55/108 (50%)	0.026	
		(229)					
		3 742–1059	<i>Photobacterium luminescens</i> insecticidal toxin complex protein TcbA (2504)	16/45 (35%)	23/45 (50%)	3.9	
		(105)					
		4 2305–2532	—	—	—	—	
		(75)					
		5 2958–3182	—	—	—	—	
		(74)					
		6 1837–2001	<i>Bacillus subtilis</i> ATP synthase (subunit i) (127)	12/28 (42%)	19/28 (67%)	5.3	
		(54)					
94	6627	1 3407–5047	<i>Rattus norvegicus</i> alpha actinin (892)	39/149 (26%)	69/149 (46%)	0.078	
		(546)					
		2 1–1231	<i>Lactococcus lactis</i> phage BK5-T ORF266; putative (266)	39/176 (22%)	78/176 (44%)	9e-05	
		(410)					
		3 2122–3111	AcNPV viral capsid associated protein (hypothetical 42.1 kDa protein in LEF8-FP intergenic region) (365)	73/294 (24%)	123/294 (41%)	2e-05	
		(329)					
		4 5065–5778	<i>Echinococcus granulosus</i> antigen II/3 (559)	43/162 (26%)	79/162 (48%)	0.009	
		(237)					
		5 5037–5744	<i>Schizosaccharomyces pombe</i> serine-rich protein (534)	46/188 (24%)	82/188 (43%)	0.012	
		(235)					
		6 1497–2132	<i>Populus balsamifera</i> subsp. <i>trichocarpa</i> laccase (437)	37/127 (29%)	54/127 (42%)	0.51	
		(211)					
		7 5920–6516	AcNPV 33 kDa early protein homolog (P33) AcOrf-92 peptide (259)	32/133 (24%)	56/133 (42%)	4e-04	
		(198)					
		8 1530–2069	<i>Mus musculus</i> GABA-B1a receptor (960)	16/59 (27%)	29/59 (49%)	8.7	
		(179)					
		9 1505–1810	Homo sapiens S6 kinase-related kinase (482)	24/68 (35%)	32/68 (46%)	0.14	
		(101)					
		10 2957–3199	<i>Serratia odorifera</i> outer membrane protein II (243)	11/26 (42%)	18/26 (68%)	6.8	
		(80)					
		11 2195–2401	<i>Schizosaccharomyces pombe</i> conserved hypothetical protein (634)	14/27 (51%)	18/27 (65%)	1.7	
		(80)					
		12 2389–2628	Homo sapiens Na+-dependent purine specific transporter (658)	12/26 (46%)	18/26 (69%)	3.0	
		(79)					
		13 1–240	Homo sapiens insulin-like growth factor binding protein precursor (258)	28/87 (32%)	33/87 (37%)	7.1	
		(79)					
		14 402–629	<i>Saccharomyces cerevisiae</i> probable membrane protein YLR194c-yeast (254)	15/43 (34%)	23/43 (52%)	0.15	
		(75)					
94		15 3200–3406	<i>Trypanosoma brucei</i> protease precursor (450)	12/32 (37%)	17/32 (52%)	5.0	
		(68)					
		16 3738–3926	—	—	—	—	
		(62)					
		17 289–483	—	—	—	—	
		(61)					
		18 2878–3048	Homo sapiens lutropin/choriogonadotropin receptor (685)	12/37 (32%)	20/37 (53%)	6.9	
		(56)					
		19 4441–4599	Rabbit hemorrhagic disease virus, capsid structural protein VP60 (579)	9/21 (42%)	15/21 (70%)	7.0	
		(52)					
117	6682	1 1726–3366	<i>Rattus norvegicus</i> alpha actinin (892)	39/149 (26%)	69/149 (46%)	0.1	
		(546)					
		2 4239–5351	AcNPV 33 kDa early protein homolog (P33), AcORF-92 peptide (259)	36/140 (25%)	65/140 (45%)	5e-06	
		(370)					
		3 441–1430	AcNPV hypothetical 42.1 kDa protein in PROTEIN IN LEF8-FP intergenic region, viral capsid associated protein (365)	73/294 (24%)	123/294 (41%)	2e-05	
		(329)					
		4 3384–4097	<i>Arabidopsis thaliana</i> putative protein (577)	28/83 (33%)	42/83 (49%)	0.012	
		(237)					

TABLE 12-continued

SEQ ID NO.	Length (nt)	Position SEQ aa)	Best Match (length, aa)	aa Identities	aa Positive	E Value
117	5	5656-6354 (232)	<i>Cricetulus griseus</i> DNA repair protein XRCC1 (633)	17/41 (41%)	25/41 (60%)	0.32
	6	1-466 (155)	<i>Pneumocystis carinii</i> KEXIN (671)	16/34 (47%)	19/34 (55%)	0.064
	7	5206-5649 (147)	<i>Arabidopsis thaliana</i> acetolactate synthase (670)	25/72 (34%)	34/72 (46%)	2.6
	8	6354-6743 (129)	Human papillomavirus type 12E7 protein (103)	17/52 (32%)	27/52 (51%)	1.0
	9	62-64-6638 (124)	<i>Eschenchia coli</i> Exodeoxyribonuclease VIII (EC 3.1.11.-) (Exo VIII), (797)	20/77 (25%)	36/77 (45%)	0.9
	10	3356-3715 (119)	<i>Saccharomyces cerevisiae</i> a-agglutinin core subunit, ORF YNR044w (725)	32/94 (34%)	42/94 (44%)	0.24
	11	6807-7154 (115)	<i>Mus musculus</i> sodium channel 25 (309)	15/58 (25%)	26/58 (43%)	1
	12	406-720 (104)	<i>Schizosaccharomyces pombe</i> conserved hypothetical protein (634)	14/27 (51%)	18/27 (65%)	2.5
	13	5761-6036 (91)	<i>Escherichia coli</i> hypothetical 77K protein (spoT 3' region) (685)	13/33 (39%)	21/33 (63%)	8.7
	14	1276-1518 (80)	<i>Serratia odorifera</i> outer membrane protein II (243)	11/26 (42%)	18/26 (68%)	6.8
	15	708-947 (79)	Homo sapiens Na ⁺ dependent purine specific transporter (658)	12/26 (46%)	18/26 (69%)	3.0
	16	6740-6976 (78)	Human papillomavirus type 2a, probable E4 protein (132)	14/47 (29%)	26/47 (54%)	0.89
	17	170-388 (72)	<i>Candida albicans</i> DNA-directed DNA polymerase III (EC 2.7.7.7) (1038)	17/55 (30%)	30/55 (53%)	6.5
	18	3851-4063 (70)	<i>Schizosaccharomyces pombe</i> hypothetical protein (962)	16/67 (23%)	32/67 (46%)	1.7
	19	1519-1725 (68)	<i>Trypanosoma brucei</i> protease precursor(450)	12/32 (37%)	17/32 (52%)	5.0
	20	2057-2254 (62)	—	—	—	—
	21	7036-7211 (58)	—	—	—	—
	22	197-1367 (56)	Homo sapiens lutropin/choriogonadotropin receptor (685)	12/37 (32%)	20/37 (53%)	6.9
	23	2760-2918 (52)	—	—	—	—
	24	5909-6064 (51)	Homo sapiens KIAA0306 (1451)	17/49 (34%)	24/49 (48%)	3.1

SEQUENCE LISTING

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gag caa gtg ttt acc gat ccc att tcg gac aac gtt acg tac acc att Glu Gln Val Phe Thr Asp Pro Ile Ser Asp Asn Val Thr Tyr Thr Ile 95 100 105 110	337
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gtg aag caa agt ttg cct cca cgc aag cgc gcc tac aat aaa gtg gtt Val Lys Gln Ser Leu Pro Pro Arg Lys Arg Ala Tyr Asn Lys Val Val	415	420	1297
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Lys Gly Ser Lys Gln Phe	
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Arg Ala Gln Asp Leu Pro Pro Asp Glu Tyr Lys Asp Leu Leu Lys Glu	
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305	310	315
Tyr Ile Glu Val Leu Val Asn Val Asp Glu Met Pro Gln Arg Ser Arg		
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Thr Cys Ser Arg Ser Ser Ser Ser Ser Ser Ser Glu Ser Asp		
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Pro Ala Lys Val Lys Val Ser Ser Pro Thr Arg Ala Pro Ala Val Ala		
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Glu Val Thr Ser Ser Thr Pro Thr Arg Ala Gln Thr Pro Pro Glu Ser		
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Val Ala Pro Thr Val Ala Lys Val Lys Gly Gly Pro Pro Lys Val Lys		
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Gln Ser Leu Pro Pro Arg Lys Arg Ala Tyr Asn Lys Val Val Glu Asp		
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<212> TYPE: PRT

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30		
Ala Trp Glu Leu His Asp Gly Thr Phe Val Leu Leu Glu Arg Arg Asp		
35	40	45
45		
Asp Ser Ser Val Asp Thr Ser Tyr Ile Gly Ala Pro Ser Ser Arg Leu		
50	55	60
60		
Thr Val Val Gln Thr Glu Ala Val Leu Lys Lys Leu Asn Val Leu Asp		
65	70	75
75		
80		
Trp Ser Trp Ala Gln Ile Val Leu Leu Asp Asn Pro Val Lys Tyr Pro		
85	90	95
95		
Gln Tyr Ser Arg Pro Thr Ile Tyr Phe Asn Tyr Val Lys Met Arg Asn		
100	105	110
110		
Cys Thr Leu Tyr Gly Gly His Val Arg Thr Leu Gly Asp Pro Val Leu		
115	120	125
125		
Tyr Leu Glu Asn Cys Ser Gly Glu Glu Val Arg Ala Leu His Ser Ser		
130	135	140
140		
Leu Ser Ser Arg Arg Tyr Cys Val Gly Phe Ala Ile Leu Thr Thr Thr		
145	150	155
155		
160		
Gly Glu Leu Arg Trp Cys Val Ser Asp Gln Ser Leu Val Lys Leu Phe		
165	170	175
175		

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Lys Thr Val Asp Thr Thr Ala Gly Tyr Cys Pro Lys Met Tyr Ile Ser
 180 185 190

Tyr Thr Thr Lys Arg Ile Leu Trp His Leu Trp Asn Ser Ser Ser Glu
 195 200 205

Phe Ala Leu Gln Arg Leu Gly Gly Ser His Val Ala Ala Leu Cys Leu
 210 215 220

Arg Glu Cys Ser Asp Gln Gly Ile Val Arg Ala Ile Lys Gly Ser Lys
 225 230 235 240

Gln Phe

<210> SEQ_ID NO 4

<211> LENGTH: 2446

<212> TYPE: DNA

<213> ORGANISM: mosquito baculovirus

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (1820)...(2218)

<221> NAME/KEY: CDS

<222> LOCATION: (2239)...(2445)

<221> NAME/KEY: CDS

<222> LOCATION: (323)...(490)

<400> SEQUENCE: 4

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ttaccaatgt accacccaaac cgccgttcat ctcgtgctaa gggccgtat atgttaggggg	120
aaaagtttgt gagattttgt ttataaaaaat attttttatt gtataataga aaaataaata	180
aatgttaaatc taaacactag aattttttgtt aacctttgtt agcgcaaca attcccttgtt	240
ccgagcactc ccgcaggcag agtgcagcga cgtgtgatcc tcccaaactgt tgcagcgaa	300
attccgaact cgagttccac ag atg cca caa aat gcg ctt ggt cgt gta gga	352
Met Pro Gln Asn Ala Leu Gly Arg Val Gly	
1 5 10	

aat gta cat ctt ggg gca gta tcc ggc ggt ggt gtc aac ggt ttt gaa	400
Asn Val His Leu Gly Ala Val Ser Gly Gly Val Asn Gly Phe Glu	
15 20 25	

cag ttt aac caa act ttg atc cga tac gca cca cct gag ctc acc ggt	448
Gln Phe Asn Gln Thr Leu Ile Arg Tyr Ala Pro Pro Glu Leu Thr Gly	
30 35 40	

ggt ggt gag tat ggc aaa tcc gac gca gta cct gcg gct cga	490
Gly Gly Tyr Gly Lys Ser Asp Ala Val Pro Ala Ala Arg	
45 50 55	

taagctagag tgcagcgcgc ggacctccctc gccgctacaa tttccaagt agagtacggg	550
gtcgccccagt gtgcgcacgt gtccaccgtt tagggtagc ttgcgcacatct tgacgttagtt	610
gaagtagatg gttggccctcg agtactgcgg gtacttgacc ggattgtcga gcagcacaat	670
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ggtttagccctc gacgaagggtg caccaatgtt gctcgtgtcc accgaggagt cgtccctcgc	790
ctccaaacgc acaaagggtt catcgtgttag ctccaaagct tggcaattt tcaagctcagc	850
gtcacacgcac tcaatggact gacgggttgg gtcgcagata cagggcttgt gacacgtac	910
aagaagacac gacattgtat tgatccctat tttattacaa atgtgcacccc accaccccaag	970
atcaccgttt atatcaccgt taaaatttaa tatcaagatt atatatattt atgtgtgttg	1030
tatatttttt tttttcttta acgtttacgt ttatataaccc gtcacttcc cttggcattt	1090
cgagactttc ggcgcacgttt agcgggctga ggtgggtggtt gcggttgcgc ctcatcttca	1150
accactttat tggtaggcgc cttgcgttggaa ggcacaaacttt gcttcacattt gggcggacca	1210

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cctttaactt tggcacagt tggccaca cttcggtg gcgttgagc ccgggtcg 1270
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gccggagctg gatctggagc tgggttggg gtctattcat cttcaactt actatcgat 1390
tccgagctcg aacttggagct gctgttagac cgtaacagg tgcgcaacg ttgtggcatt 1450
tcatccacgt tgacaaaac ttcatgttat tcattctta cgattcctg cgacacggcc 1510
ggtccacgt ccacggctg ttctgtca tcttaaaagt ttcaagttt ttgaatcaa 1570
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cccttaaaact tggcacctt ccgttgaccg gcagatgtc gcttagccac cgtaataatc 1690
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aaattgtaat cgctcagcgt agtttacgg cgataatat cctcatcgta gtcctcgta 1810
ggtccgtac atg tgc cgt gga cag tcg ggg ttt cca cga ttg cga att tcg 1861
Met Cys Arg Gly Gln Ser Gly Phe Pro Arg Leu Arg Ile Ser
60 65 70
tac tcc ttg agc aaa tcc ttg tac tca tcg ggg ggt aaa tct tgc gca 1909
Tyr Ser Leu Ser Lys Ser Leu Tyr Ser Ser Gly Gly Lys Ser Cys Ala
75 80 85
cga ata acg ata gcc ttg tcg ccc gag ccc gac ccc att ccc gac ttg 1957
Arg Ile Thr Ile Ala Leu Ser Pro Glu Pro Asp Pro Ile Pro Asp Leu
90 95 100
gaa agc ctg ata gac tcc tcg atc atg tac tgg gat ttg cgg cgc gcc 2005
Glu Ser Leu Ile Asp Ser Ser Ile Met Tyr Trp Asp Leu Arg Arg Ala
105 110 115
aac atc atc gta aac gtt tcc gga tac tcg gag ggc aca acc gcg cgc 2053
Asn Ile Ile Val Asn Val Ser Gly Tyr Ser Glu Gly Thr Thr Ala Arg
120 125 130
ata tta ttg agc cca gag tcg gtg aat acg tgc acc cgc gtc aca atg 2101
Ile Leu Leu Ser Pro Glu Ser Val Asn Thr Cys Thr Arg Val Thr Met
135 140 145 150
cta tcc gta atg gtg tac gta acg ttg tcc gaa atg gga tcg gta aac 2149
Leu Ser Val Met Val Tyr Val Thr Leu Ser Glu Met Gly Ser Val Asn
155 160 165
act tgc tcg att ttt aaa att ctc aac agg tcc cgg tgt ccg ctc ata 2197
Thr Cys Ser Ile Phe Lys Ile Leu Asn Arg Ser Arg Cys Pro Leu Ile
170 175 180
aag ccg ggg ttg agt cca ccg tgaaccgcag caaacacgcg ctg cac cac gag 2250
Lys Pro Gly Leu Ser Pro Pro Leu His His Glu
185 190
gtt gaa ggg aag agt gct acg ctg ggc gcc gta ctc gac ctc aat tac 2298
Val Glu Gly Lys Ser Ala Thr Leu Gly Ala Val Leu Asp Leu Asn Tyr
195 200 205
aat ctg tcg act gtt tgg tgc agc ctt cgc ttt aat ttc gtt ggt cca 2346
Asn Leu Ser Thr Val Trp Cys Ser Leu Arg Phe Asn Phe Val Gly Pro
210 215 220 225
cgc ctc aca gcc aac gtt cgt ggc gac cca aac ggt cgt gta cac atc 2394
Arg Leu Thr Ala Asn Val Arg Gly Asp Pro Asn Gly Arg Val His Ile
230 235 240
ccc cac gtc cgg aaa cga agg tgg caa aat tgg cat ctc gtt cat cga 2442
Pro His Val Arg Lys Arg Arg Trp Gln Asn Trp His Leu Val His Arg
245 250 255
att c 2446
Ile

<210> SEQ ID NO 5

<211> LENGTH: 56

<212> TYPE: PRT

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<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 5

Met Pro Gln Asn Ala Leu Gly Arg Val Gly Asn Val His Leu Gly Ala

1 5 10 15

Val Ser Gly Gly Val Asn Gly Phe Glu Gln Phe Asn Gln Thr Leu

20 25 30

Ile Arg Tyr Ala Pro Pro Glu Leu Thr Gly Gly Glu Tyr Gly Lys

35 40 45

Ser Asp Ala Val Pro Ala Ala Arg

50 55

<210> SEQ ID NO 6

<211> LENGTH: 133

<212> TYPE: PRT

<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 6

Met Cys Arg Gly Gln Ser Gly Phe Pro Arg Leu Arg Ile Ser Tyr Ser

1 5 10 15

Leu Ser Lys Ser Leu Tyr Ser Ser Gly Gly Lys Ser Cys Ala Arg Ile

20 25 30

Thr Ile Ala Leu Ser Pro Glu Pro Asp Pro Ile Pro Asp Leu Glu Ser

35 40 45

Leu Ile Asp Ser Ser Ile Met Tyr Trp Asp Leu Arg Arg Ala Asn Ile

50 55 60

Ile Val Asn Val Ser Gly Tyr Ser Glu Gly Thr Thr Ala Arg Ile Leu

65 70 75 80

Leu Ser Pro Glu Ser Val Asn Thr Cys Thr Arg Val Thr Met Leu Ser

85 90 95

Val Met Val Tyr Val Thr Leu Ser Glu Met Gly Ser Val Asn Thr Cys

100 105 110

Ser Ile Phe Lys Ile Leu Asn Arg Ser Arg Cys Pro Leu Ile Lys Pro

115 120 125

Gly Leu Ser Pro Pro

130

<210> SEQ ID NO 7

<211> LENGTH: 69

<212> TYPE: PRT

<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 7

Leu His His Glu Val Glu Gly Lys Ser Ala Thr Leu Gly Ala Val Leu

1 5 10 15

Asp Leu Asn Tyr Asn Leu Ser Thr Val Trp Cys Ser Leu Arg Phe Asn

20 25 30

Phe Val Gly Pro Arg Leu Thr Ala Asn Val Arg Gly Asp Pro Asn Gly

35 40 45

Arg Val His Ile Pro His Val Arg Lys Arg Arg Trp Gln Asn Trp His

50 55 60

Leu Val His Arg Ile

65

<210> SEQ ID NO 8

<211> LENGTH: 53

<212> TYPE: PRT

<213> ORGANISM: mosquito baculovirus

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<400> SEQUENCE: 8

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Met Asn Thr Ser Lys Phe Trp Ser Thr Trp Met Lys Cys His Asn Val
 1           5          10          15

Arg Ala Pro Val His Gly Leu Ala Ala Ala Pro Val Arg Ala Arg Asn
20          25          30

Pro Ile Val Lys Val Arg Met Asn Arg Pro Gln Pro Gln Leu Gln Ile
35          40          45

Gln Leu Arg Arg Arg
50

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<210> SEQ ID NO 9

<211> LENGTH: 64

<212> TYPE: PRT

<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 9

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Lys Gly Arg Val Leu Arg Trp Ala Pro Tyr Ser Thr Ser Ile Thr Ile
 1           5          10          15

Cys Arg Leu Phe Gly Ala Ala Phe Ala Leu Ile Ser Leu Val His Ala
20          25          30

Ser Gln Pro Thr Phe Val Ala Thr Gln Thr Val Val Tyr Thr Ser Pro
35          40          45

Thr Ser Gly Asn Glu Gly Gly Lys Ile Gly Ile Ser Phe Ile Glu Phe
50           55          60

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<210> SEQ ID NO 10

<211> LENGTH: 6624

<212> TYPE: DNA

<213> ORGANISM: mosquito baculovirus

<220> FEATURE:

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<221> NAME/KEY: CDS
<222> LOCATION: (2630)...(3334)
<221> NAME/KEY: CDS
<222> LOCATION: (11)...(541)
<221> NAME/KEY: CDS
<222> LOCATION: (5333)...(5848)
<221> NAME/KEY: CDS
<222> LOCATION: (5892)...(6188)
<221> NAME/KEY: CDS
<222> LOCATION: (4458)...(4739)
<221> NAME/KEY: CDS
<222> LOCATION: (2243)...(2473)
<221> NAME/KEY: CDS
<222> LOCATION: (6432)...(6620)
<221> NAME/KEY: CDS
<222> LOCATION: (3865)...(4044)

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<400> SEQUENCE: 10

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gaattctctc atg ata acg ggg tat ata aag gtt ggt ttc ggg gct cgg      49
      Met Ile Thr Gly Tyr Ile Lys Val Gly Phe Gly Ala Arg
        1           5          10

```

```

ctg gaa cct agc agc atg aat cga aag cgg cta act aaa ttc gtg cgc      97
Leu Glu Pro Ser Ser Met Asn Arg Lys Arg Leu Thr Lys Phe Val Arg
15          20          25

```

```

gac ttg tat cgc gag ttt aat gag gtt cac tgc gaa cag aga ctg gaa      145
Asp Leu Tyr Arg Glu Phe Asn Glu Val His Cys Glu Gln Arg Leu Glu
30          35          40          45

```

```

gcg tta gac cgc gct gtg gac gcc gaa acg gag ggt att tat ctt ggg      193
Ala Leu Asp Arg Ala Val Asp Ala Glu Thr Glu Gly Ile Tyr Leu Gly
50           55          60

```

```

ctt agt gtg cgc aat cgt tac agt cat cgg gtg gtt tac cgg gca tgg      241
Leu Ser Val Arg Asn Arg Tyr Ser His Arg Val Val Tyr Arg Ala Trp
65           70          75

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atc gag cgt ggg gtc gcg cag cgg aac tgg ttt tgt gaa att gaa tta	289
Ile Glu Arg Gly Val Ala Gln Arg Asn Trp Phe Cys Glu Ile Glu Leu	
80 85 90	
cca caa gcg gtg ctc gac gct aac cat tac att tta att tat ttc ggc	337
Pro Gln Ala Val Leu Asp Ala Asn His Tyr Ile Leu Ile Tyr Phe Gly	
95 100 105	
aca cga gtc tat tgc caa cag ccg tgg cta acg tac ctg gac aaa acg	385
Thr Arg Val Tyr Cys Gln Gln Pro Trp Leu Thr Tyr Leu Asp Lys Thr	
110 115 120 125	
tac aag tgt tgg ggt aat agt gca cga caa cca act ccg tcg gaa ctg	433
Tyr Lys Cys Trp Gly Asn Ser Ala Arg Gln Pro Thr Arg Ser Glu Leu	
130 135 140	
aag cgc gta cct agc acc tac tgg cgc cac aac acc acc tat ata acg	481
Lys Arg Val Pro Ser Thr Tyr Trp Arg His Asn Thr Thr Tyr Ile Thr	
145 150 155	
atg gac gcg cga tca ttt cga cca ctt gtc cgc ttc atg atc gac gtc	529
Met Asp Ala Arg Ser Phe Arg Pro Leu Val Arg Phe Met Ile Asp Val	
160 165 170	
cac gat gaa cgc tgactgtttc tgcccacccg gaccctgcta ccatgcactc	581
His Asp Glu Arg	
175	
ttcagccact gcggaggat ctgccagtc tggtggAACCC actacgaaga cctagacgag	641
ttcgtgcgt gtatggggg ccagaccacc cacaaccga accccatgc cataacaatg	701
gggctctgcg aatactgtcc gagaaggcac ccggtcggcg tgcctgcca aggctatcca	761
gcgtgcgaaa aatgtccct gtgcacgccc ccactcccc aatgtccccc ccgattaagc	821
ctatatttct ttctttcaa gaaaaataat aaaaaatgt aaaaattata cacctcgttt	881
tattgcagca gtaaaatat cactccctt ccagcacctt caagcgttg tccatcgttt	941
tgatactgtc gcccaactca ttgatggcga cgttatgtt tgaaaattta tcatcactgg	1001
agctggacag ctccgacagg tcgtcggtca gttgcccaa ggtgggttca atggggccaa	1061
gctttgctc gagctcggtcc actctagccg ttagtttgtt gaggtccacc cccgagccct	1121
cctcgactt gcactcgaaa ggttgggctg ggtagcgcatt gatgagcacg gccaccattt	1181
tgaccatgt tagtagaatt agaaatagt aagtttgggg catcggttgc tcttacttgc	1241
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ctccaccagc tcgccccata tattctccaa tggccgttgc attgcgttca aattttccac	1421
acccgaccgt tcgacactcgat caatcgctg ctccgtgtcg ctcaactgtt gtcgggttgc	1481
ggtaacgcgc tccttcaatg gggacaggc cggcaaatgg tcgtccccac attcacgtt	1541
ggcacccctt acggtaaga ttgtatcgat ggtcattatc gttacatgg tcagtataaa	1601
aattaaaaat attacaagggt gtgacgacat cgtgaggctt atggcgggga acaggtgcac	1661
cgtgagacca accgcacgg accgaaaccc tccagggtgt cctcgagtaa ccggccgtca	1721
acggtcacca ccgcgggccc cggtcgatc accaaataca ctccgtactc acaggcaccc	1781
atataactga tctcgctgtc cccctctgtt agcacaat tccgcggta gaagcgccgt	1841
ttgcgcaggat tccgcaccac aatatacaacc gagactcgac acatgttacg cccgctcgta	1901
aactcgctt acgcacgcac cttgtcgctt ggtcaaggcac accggaaatgg ggcgattata	1961
cgccccccggg cggttaatgt atttcgttgtt accagtcggccg cacacacaag cgtccggag	2021
gaacgttgc tcgagcaagt ttatctccaa ttgaccgcgcg gtacacacat acggttgcag	2081

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tttgttatcg tcggtaaaaa tgcgcgata ggttggaaagg caggattgtatataacgaa	2141
ttcgtctgca gtgaatcccc gtaaaaattcc atgcttctcg acacaatttc gtttctcgaa	2201
aatagattta tgatccgtgc tgccagaaccc gcctatgcac g atg aaa ctc ctc cgt Met Lys Leu Leu Arg 180	2257
ctc tgg tca aag cgc agt tac gtt gac agt ccg cat tat caa tac acg Leu Trp Ser Lys Arg Ser Tyr Val Asp Ser Pro His Tyr Gln Tyr Thr 185 190 195	2305
gta att tgg tgt tgg ggc aat cta cgt gct gag agc ccg cga aat gaa Val Ile Trp Cys Cys Gly Asn Leu Arg Ala Glu Ser Arg Arg Asn Glu 200 205 210	2353
tct ctg gca gca ccg att cac ccc gag ctc gtg ccg ccc gtt ccc ccg Ser Leu Ala Ala Pro Ile His Pro Glu Leu Val Arg Pro Val Pro Ala 215 220 225 230	2401
act ctt ggg cgt gtt tgg cta gaa att ttg cac ccg aag tta aaa tca Thr Leu Gly Arg Val Trp Leu Glu Ile Leu His Pro Lys Leu Lys Ser 235 240 245	2449
act gaa tca tta cga gca cca gta tgagcaccac taaaaccgtac aacatttttt Thr Glu Ser Leu Arg Ala Pro Val 250	2503
ccctttctat ttccacagga atcccaactt aaagacattt ggaacacttt cgagaagccc	2563
gaggagcgca aatggccct tcagctaaggc gacaagggtgt gtttgcacc ggaagaattc	2623
gacaca atg agt gaa ttc atc gag acc gta cac tac aac acc gac ccg Met Ser Glu Phe Ile Glu Thr Val His Tyr Asn Thr Asp Pro 255 260 265	2671
atc cgg tcg agc tat ggc att tgt ggg ctg cac acc ccg ggg aac ccg Ile Arg Ser Ser Tyr Gly Ile Cys Gly Leu His Thr Arg Gly Asn Arg 270 275 280	2719
ggc tgc cga gag tgg gtg att gat atc gat ttg aaa act gac gac ccc Gly Cys Arg Glu Trp Val Ile Asp Ile Asp Leu Lys Thr Asp Asp Pro 285 290 295 300	2767
gag ttg gcc aac ttt gtg ctc aac gtg tcc gtg gtc acc tca atg ttc Glu Leu Ala Asn Phe Val Leu Asn Val Ser Val Val Thr Ser Met Phe 305 310 315	2815
ttc ttc ggt acc gaa aac att aaa gtt tac cac acg ggc aac gac ggc Phe Phe Gly Thr Glu Asn Ile Lys Val Tyr His Thr Gly Asn Asp Gly 320 325 330	2863
atc cac att tgg ctc aac ccg gcc aac ttc ccg gtg gac tcg agc gcc Ile His Ile Trp Leu Asn Pro Ala Asn Phe Pro Val Asp Ser Ser Ala 335 340 345	2911
gaa ttg cgc gga ttc tac ctc gcc gcc atg cag cta ccc aaa ggt gag Glu Leu Arg Gly Phe Tyr Leu Ala Ala Met Gln Leu Pro Lys Gly Glu 350 355 360	2959
gag gaa cta cac gag ctg gtg ccg acc acc gag tgc agg ttg ttt tgc Glu Glu Leu His Glu Leu Val Arg Thr Thr Glu Cys Arg Leu Phe Cys 365 370 375 380	3007
gac gcc gac tgc tgc gga atc gat tgc aag ccc aag atg cgc atc atc Asp Ala Asp Cys Cys Gly Ile Asp Cys Lys Pro Lys Met Arg Ile Ile 385 390 395	3055
gac acc cca ccc aat ccc acg gaa ccg att tcg ttt gcc gag tgc ttt Asp Thr Pro Pro Asn Pro Thr Glu Pro Ile Ser Phe Ala Glu Cys Phe 400 405 410	3103
gtg cgc gct ctc tgc tgc aac gaa acc tat atg aac gaa atg aca tcg Val Arg Ala Leu Cys Cys Asn Glu Thr Tyr Met Asn Glu Met Thr Ser 415 420 425	3151
att ata cgc aac aac ccg gac gtg gtg agc acc gtc acc gac gtg tgg Ile Ile Arg Asn Asn Arg Asp Val Val Ser Thr Val Thr Asp Val Trp 430 435 440	3199

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aga ctc ttt tgg ccg ccc ata gat gcg ggc ctg ttt caa tcg cca gct Arg Leu Phe Trp Pro Pro Ile Asp Ala Gly Leu Phe Gln Ser Pro Ala 445 450 455 460	3247
aga ctc tgc cgt gca ccc ctc agt tac cac ttg aag ggc ggt cggtt Arg Leu Cys Arg Ala Pro Leu Ser Tyr His Leu Lys Gly Gly Arg Leu 465 470 475	3295
tcg cgt cgt att gag ttg gat gaa tat ttt aaa aat gat tgaaataaaa Ser Arg Arg Ile Asp Leu Asp Glu Tyr Phe Lys Asn Asp 480 485	3344
agttttatta acaatgactc attgaagttt ttattcccc caacatcaca agttcaaccc cgactgcggc tccatataat gaaaaatgtt catttggtag caccactta acgggtccac ttttgtgggg ccgc当地atg ttgggctcca tatggaaaag tttagccaaac caagacgggt ccactttgtt gggcccaca ttgcgggtc taaaggggtt gggttttgtt tgaaataaaa taaaaaatttt ctaactctaa caggatttat tatatttgat cacatttttc atcacaacat tagcgcgggtg tggcgtttt atcacagata gaccaccgc gaatcgtaca cactggccgc tcttttaggtc gacgttcaca cagtgcacca agttgcaacg ctgtccagtt cgggtcagta ccaccatacg agcctcccaa taatgttcca gcagaatctt tgcaagatcg cggtgatttt taatatcgag caatagcacc accggaccgt tgaccgtAAC atg gtt gag ctg acg Met Val Glu Leu Thr 490	3404 3464 3524 3584 3644 3704 3764 3824 3879 3927 3975 4023 4074 4134 4194 4254 4314 4374 4434 4487 4535 4583 4631 4679
aat tgc agt gcc aaa gtc tcc agt ata gtg gta cca aca ttg gct aac Asn Cys Ser Ala Lys Val Ser Ser Ile Val Val Pro Thr Leu Ala Asn 495 500 505 510	
gtt att cac caa tac cat cca agt ttc gtg cag ggc tgc gtc aac Val Ile His Gln Tyr His Pro Ser Phe Val Gln Ala Ser Gly Val Asn 515 520 525	
tat ggt gct aaa aag ttt caa atc tac cag caa att tgt gca ctc gtt Tyr Gly Ala Lys Phe Gln Ile Tyr Gln Gln Ile Cys Ala Leu Val 530 535 540	
aac cag gtc cgg gtc gca tga aagtaacacc aagttgtggg cactagcggc Asn Gln Val Arg Val Ala *545	
gcgtataatt tgctcccgca gtacccctcg cggatacgcac gcgacaagca ttgaacagcg attccaaacaa cttggctcg aagcacctcg actcgataac ccagtggtcc gtagttgggt gatagaatcc gtcaaaagcga ccttttctc tcagttccag cggcgtgagc ggtcgaaagg tataaaaattt ctcctgaact gtggcgtacc ataagagagg atcggtttta cgagcgacat tcataacctc cccgttata ggcaaaagtgt cgaggtgaaa ccagtttagat tgagcgttat tacggccaaa cacgaccgcg cagtcgcacat cacgaacata caaatccatc cttatcaccg cagaccgggtg gagtcatgtg acc atg ccc ttg gtg cac att gaa cag cgc gga Met Pro Leu Val His Ile Glu Gln Arg Gly 550 555	
ttg tcg tgc tat gtc gct ggt ttc gag gcc aac gtg gaa ccc gac ctg Leu Ser Cys Tyr Val Ala Gly Phe Glu Ala Asn Val Glu Pro Asp Leu 560 565 570	
tac cag tgt att gtc gat tgc aaa ccc cac ctt atg cgc tat ata gca Tyr Gln Cys Ile Val Asp Cys Lys Pro His Leu Met Arg Tyr Ile Ala 575 580 585 590	
ctt aac cat ccg gaa ttt ttc gca cag ctg agg cca atc gat ggg cac Leu Asn His Pro Glu Phe Phe Ala Gln Leu Arg Pro Ile Asp Gly His 595 600 605	
aac ctt tac agt tcc acc agt ggg gat tac atc gat cta tgg ctt gag Asn Leu Tyr Ser Ser Thr Ser Gly Asp Tyr Ile Asp Leu Trp Leu Glu	

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610	615	620	
cta ctg aac gag gct gct atg aag tcg ggc ttg gat gaa gag ggt gga Leu Leu Asn Glu Ala Ala Met Lys Ser Gly Leu Asp Glu Glu Gly Gly	625	630	4727
tta ggg agc tgt tgagcaaaca ttttcgcttg gaagaaaagg aagagaaaata Leu Gly Ser Cys	640		4779
aacaaacaac ttttagttac atcatcaagt gtttatttt tctaaaaactg ccctcgattt ctccaccaaa ccctccataa attgcagctc atcggggaaag catttgcga ccaggtccag			4839
cagttgcttc gcgccttagat aggcacatc gatgtttaaa cagtagccaa agtagtactc caaatctcga ctctcgtaca tcacttctgt accgtcgcac accactcgca tggagatgga			4899
ccgcagggtcc atgtcgtaat gtaaaaactag aagaaaacttt tccggtgcca atgaggtaac ttctccgtac tcgagcagct cttggggcag ctogaagggg atcatttcg gtaaacccgtg			5019
cggcgtatc aggaccgtat tttcgtgcca ctcccactcg gcgggcgaca ttagggccaa atcgtggccc gctgccgtta cgttgccaaa gctgctatTTT atgttgttagg cttcgtactg			5079
tacgaagccc cgacccgcca actgggtggc cacgtataaa aatctcgtca acgggtggcg caggtaccga aag atg gtt cga cga ttt tca gct cca acg tgc aca aat			5139
Met Val Arg Arg Phe Ser Ala Pro Thr Cys Thr Asn 645 650			5368
gta ccc gaa aag ctg tac atg ttt gcg gtg aag ttc agc tac tct tta Val Pro Glu Lys Leu Tyr Met Phe Ala Val Lys Phe Ser Tyr Ser Leu	655	660	5416
665 670			
aaa tat cgt act ata aat cga ttc acg ctc acc aat cgt agc agt att Lys Tyr Arg Thr Ile Asn Arg Phe Thr Leu Thr Asn Arg Ser Ser Ile	675	680	5464
685			
cac aca atg ttg tac tct gta gaa gtt cgc gta ttt agt acg gag att His Thr Met Leu Tyr Ser Val Glu Val Arg Val Phe Ser Thr Glu Ile	690	695	5512
695 700			
ccg tcg cag tcg ctg cac cac tcc cac cat atc gcc ata ccg ttc gat Pro Ser Gln Ser Leu His His Ser His Ile Ala Ile Pro Phe Asp	705	710	5560
715			
aaa gat aga tgg acc gtc gat ggc att tta ccg aac gat ata ccg ctc Lys Asp Arg Trp Thr Val Asp Gly Ile Leu Pro Asn Asp Ile Pro Leu	720	725	5608
730			
gac cac acg ata ccg ttg tgt gtt acc gtc agg ggt agt aaa aaa ttt Asp His Thr Ile Arg Leu Cys Val Thr Val Arg Gly Ser Lys Lys Phe	735	740	5656
745 750			
tcc tgc gta tgg cga gag acc acc tac aag tgc gga aat gtg tac gat Ser Cys Val Trp Arg Glu Thr Thr Tyr Lys Cys Gly Asn Val Tyr Asp	755	760	5704
765			
cca cca cta gag tac cag ttg gag aag ctg ccg ggc gtg cag tat agc Pro Pro Leu Glu Tyr Gln Leu Glu Lys Leu Pro Gly Val Gln Tyr Ser	770	775	5752
780 785			
gat cta gcg tta agg ata atc gag aag ttt gag cgc gct atg aag tac Asp Leu Ala Leu Arg Ile Ile Glu Lys Phe Glu Arg Ala Met Lys Tyr	785	790	5800
795			
acg ata gaa gtc gat ttc act gca aat aaa tct caa agt ttg gaa tta Thr Ile Glu Val Asp Phe Thr Ala Asn Lys Ser Gln Ser Leu Glu Leu	800	805	5848
810			
taaaccaccc gtcttcatt gttaacccgc ccgcaacccca acg atg tta caa gtt Met Leu Gln Val	815		5903
tcc cta gta gga ccc cac ttc aca ctc gtg ctc gcc agt ggc gat ttg Ser Leu Val Gly Pro His Phe Thr Leu Val Leu Ala Ser Gly Asp Leu	820	825	5951
830			

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cggtgc cag ttt cta tta cca ccg tgg gcc gca ctg gac aac agt ttg Arg Cys Gln Phe Leu Leu Pro Pro Trp Ala Ala Leu Asp Asn Ser Leu 835 840 845 850	5999
atg ctc gtc gtg cag tgg gat cag cgc aac tat acc ctc aac tgg gcg Met Leu Val Val Gln Trp Asp Gln Arg Asn Tyr Thr Leu Asn Trp Ala 855 860 865	6047
ggc gaa ata ttt tac ggt gga att gca gca cga ccg gtg aca ccg cac Gly Glu Ile Phe Tyr Gly Gly Ile Ala Ala Arg Pro Val Thr Pro His 870 875 880	6095
atg ctc aag tgg tgc tac cac ctc gcg gtc cac cct gag ccc aac ttt Met Leu Lys Trp Cys Tyr His Leu Ala Val His Pro Glu Pro Asn Phe 885 890 895	6143
acc gtg gaa gaa aaa caa cct ggc tgg gat tta cga cac cct tta Thr Val Glu Glu Lys Gln Pro Gly Cys Asp Leu Arg His Pro Leu 900 905 910	6188
taataaaaaaaa aaaatcgctt caaacaggga caataaaaacc cacaagtgtta tagagttttt tttttattttt attttcccaa gtatatttggaa actggaaaga aataataaca acaataataaa caataataat atcaataaaaaa aaggattatcg atttatgact gtgcgcgcgc gcacaacagg gccggcttct tgtttacaaa ctcaacttcc tgattctcgca ccgtagcgcc cgggagctca	6248 6308 6368 6428
tgc ttg tgc act ggt aac ctg cac ggg ata gag gaa cgt ttc cac cct Leu Cys Thr Gly Asn Leu His Gly Ile Glu Glu Arg Phe His Pro 915 920 925	6476
atc gag caa cac ccc act ttc acc gac caa ctc act caa cca tgg ccg Ile Glu Gln His Pro Thr Phe Thr Asp Gln Leu Thr Gln Pro Trp Pro 930 935 940	6524
att tgg aca cac agc tgg ggg act ttg tcg acc cgg gcc aac att tcg Ile Trp Thr His Ser Trp Gly Thr Leu Ser Thr Arg Ala Asn Ile Ser 945 950 955 960	6572
tcg ggc tcc agg tcg tgc ggt atc gta gaa tct cga aca cgg cgc caa Ser Gly Ser Arg Ser Cys Gly Ile Val Glu Ser Arg Thr Arg Arg Gln 965 970 975	6620
gctt	6624

<210> SEQ ID NO 11
<211> LENGTH: 177
<212> TYPE: PRT
<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 11

Met Ile Thr Gly Tyr Ile Lys Val Gly Phe Gly Ala Arg Leu Glu Pro 1 5 10 15
Ser Ser Met Asn Arg Lys Arg Leu Thr Lys Phe Val Arg Asp Leu Tyr 20 25 30
Arg Glu Phe Asn Glu Val His Cys Glu Gln Arg Leu Glu Ala Leu Asp 35 40 45
Arg Ala Val Asp Ala Glu Thr Glu Gly Ile Tyr Leu Gly Leu Ser Val 50 55 60
Arg Asn Arg Tyr Ser His Arg Val Val Tyr Arg Ala Trp Ile Glu Arg 65 70 75 80
Gly Val Ala Gln Arg Asn Trp Phe Cys Glu Ile Glu Leu Pro Gln Ala 85 90 95
Val Leu Asp Ala Asn His Tyr Ile Leu Ile Tyr Phe Gly Thr Arg Val 100 105 110
Tyr Cys Gln Gln Pro Trp Leu Thr Tyr Leu Asp Lys Thr Tyr Lys Cys 115 120 125

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Trp Gly Asn Ser Ala Arg Gln Pro Thr Arg Ser Glu Leu Lys Arg Val
130 135 140

Pro Ser Thr Tyr Trp Arg His Asn Thr Thr Tyr Ile Thr Met Asp Ala
145 150 155 160

Arg Ser Phe Arg Pro Leu Val Arg Phe Met Ile Asp Val His Asp Glu
165 170 175

Arg

<210> SEQ ID NO 12

<211> LENGTH: 77

<212> TYPE: PRT

<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 12

Met Lys Leu Leu Arg Leu Trp Ser Lys Arg Ser Tyr Val Asp Ser Pro
1 5 10 15

His Tyr Gln Tyr Thr Val Ile Trp Cys Cys Gly Asn Leu Arg Ala Glu
20 25 30

Ser Arg Arg Asn Glu Ser Leu Ala Ala Pro Ile His Pro Glu Leu Val
35 40 45

Arg Pro Val Pro Ala Thr Leu Gly Arg Val Trp Leu Glu Ile Leu His
50 55 60

Pro Lys Leu Lys Ser Thr Glu Ser Leu Arg Ala Pro Val
65 70 75

<210> SEQ ID NO 13

<211> LENGTH: 235

<212> TYPE: PRT

<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 13

Met Ser Glu Phe Ile Glu Thr Val His Tyr Asn Thr Asp Pro Ile Arg
1 5 10 15

Ser Ser Tyr Gly Ile Cys Gly Leu His Thr Arg Gly Asn Arg Gly Cys
20 25 30

Arg Glu Trp Val Ile Asp Ile Asp Leu Lys Thr Asp Asp Pro Glu Leu
35 40 45

Ala Asn Phe Val Leu Asn Val Ser Val Val Thr Ser Met Phe Phe Phe
50 55 60

Gly Thr Glu Asn Ile Lys Val Tyr His Thr Gly Asn Asp Gly Ile His
65 70 75 80

Ile Trp Leu Asn Pro Ala Asn Phe Pro Val Asp Ser Ser Ala Glu Leu
85 90 95

Arg Gly Phe Tyr Leu Ala Ala Met Gln Leu Pro Lys Gly Glu Glu Glu
100 105 110

Leu His Glu Leu Val Arg Thr Thr Glu Cys Arg Leu Phe Cys Asp Ala
115 120 125

Asp Cys Cys Gly Ile Asp Cys Lys Pro Lys Met Arg Ile Ile Asp Thr
130 135 140

Pro Pro Asn Pro Thr Glu Pro Ile Ser Phe Ala Glu Cys Phe Val Arg
145 150 155 160

Ala Leu Cys Cys Asn Glu Thr Tyr Met Asn Glu Met Thr Ser Ile Ile
165 170 175

Arg Asn Asn Arg Asp Val Val Ser Thr Val Thr Asp Val Trp Arg Leu
180 185 190

Phe Trp Pro Pro Ile Asp Ala Gly Leu Phe Gln Ser Pro Ala Arg Leu

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195	200	205
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Cys	Arg	Ala	Pro	Leu	Ser	Tyr	His	Leu	Lys	Gly	Gly	Arg	Leu	Ser	Arg
210				215					220						
Arg	Ile	Asp	Leu	Asp	Glu	Tyr	Phe	Lys	Asn	Asp					
225				230					235						

<210> SEQ_ID NO 14
<211> LENGTH: 59
<212> TYPE: PRT
<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 14

Met	Val	Glu	Leu	Thr	Asn	Cys	Ser	Ala	Lys	Val	Ser	Ser	Ile	Val	Val
1				5					10				15		

Pro	Thr	Leu	Ala	Asn	Val	Ile	His	Gln	Tyr	His	Pro	Ser	Phe	Val	Gln
					20			25				30			

Ala	Ser	Gly	Val	Asn	Tyr	Gly	Ala	Lys	Lys	Phe	Gln	Ile	Tyr	Gln	Gln
					35			40			45				

Ile	Cys	Ala	Leu	Val	Asn	Gln	Val	Arg	Val	Ala					
					50			55							

<210> SEQ_ID NO 15

<211> LENGTH: 94
<212> TYPE: PRT
<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 15

Met	Pro	Leu	Val	His	Ile	Glu	Gln	Arg	Gly	Leu	Ser	Cys	Tyr	Val	Ala
1					5			10				15			

Gly	Phe	Glu	Ala	Asn	Val	Glu	Pro	Asp	Leu	Tyr	Gln	Cys	Ile	Val	Asp
					20			25			30				

Cys	Lys	Pro	His	Leu	Met	Arg	Tyr	Ile	Ala	Leu	Asn	His	Pro	Glu	Phe
					35			40			45				

Phe	Ala	Gln	Leu	Arg	Pro	Ile	Asp	Gly	His	Asn	Leu	Tyr	Ser	Ser	Thr
					50			55			60				

Ser	Gly	Asp	Tyr	Ile	Asp	Leu	Trp	Leu	Glu	Leu	Leu	Asn	Glu	Ala	Ala
					65			70			75		80		

Met	Lys	Ser	Gly	Leu	Asp	Glu	Gly	Gly	Leu	Gly	Ser	Cys			
					85			90							

<210> SEQ_ID NO 16

<211> LENGTH: 172
<212> TYPE: PRT
<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 16

Met	Val	Arg	Arg	Phe	Ser	Ala	Pro	Thr	Cys	Thr	Asn	Val	Pro	Glu	Lys
1					5			10				15			

Leu	Tyr	Met	Phe	Ala	Val	Lys	Phe	Ser	Tyr	Ser	Leu	Lys	Tyr	Arg	Thr
					20			25			30				

Ile	Asn	Arg	Phe	Thr	Leu	Thr	Asn	Arg	Ser	Ser	Ile	His	Thr	Met	Leu
					35			40			45				

Tyr	Ser	Val	Glu	Val	Arg	Val	Phe	Ser	Thr	Glu	Ile	Pro	Ser	Gln	Ser
					50			55			60				

Leu	His	His	Ser	His	His	Ile	Ala	Ile	Pro	Phe	Asp	Lys	Asp	Arg	Trp
					65			70			75		80		

Thr	Val	Asp	Gly	Ile	Leu	Pro	Asn	Asp	Ile	Pro	Leu	Asp	His	Thr	Ile
					85			90			95				

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Arg Leu Cys Val Thr Val Arg Gly Ser Lys Lys Phe Ser Cys Val Trp
100 105 110

Arg Glu Thr Thr Tyr Lys Cys Gly Asn Val Tyr Asp Pro Pro Leu Glu
115 120 125

Tyr Gln Leu Glu Lys Leu Pro Gly Val Gln Tyr Ser Asp Leu Ala Leu
130 135 140

Arg Ile Ile Glu Lys Phe Glu Arg Ala Met Lys Tyr Thr Ile Glu Val
145 150 155 160

Asp Phe Thr Ala Asn Lys Ser Gln Ser Leu Glu Leu
165 170

<210> SEQ ID NO 17

<211> LENGTH: 99

<212> TYPE: PRT

<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 17

Met Leu Gln Val Ser Leu Val Gly Pro His Phe Thr Leu Val Leu Ala
1 5 10 15

Ser Gly Asp Leu Arg Cys Gln Phe Leu Leu Pro Pro Trp Ala Ala Leu
20 25 30

Asp Asn Ser Leu Met Leu Val Val Gln Trp Asp Gln Arg Asn Tyr Thr
35 40 45

Leu Asn Trp Ala Gly Glu Ile Phe Tyr Gly Ile Ala Ala Arg Pro
50 55 60

Val Thr Pro His Met Leu Lys Trp Cys Tyr His Leu Ala Val His Pro
65 70 75 80

Glu Pro Asn Phe Thr Val Glu Glu Lys Gln Pro Gly Cys Asp Leu Arg
85 90 95

His Pro Leu

<210> SEQ ID NO 18

<211> LENGTH: 63

<212> TYPE: PRT

<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 18

Leu Cys Thr Gly Asn Leu His Gly Ile Glu Glu Arg Phe His Pro Ile
1 5 10 15

Glu Gln His Pro Thr Phe Thr Asp Gln Leu Thr Gln Pro Trp Pro Ile
20 25 30

Trp Thr His Ser Trp Gly Thr Leu Ser Thr Arg Ala Asn Ile Ser Ser
35 40 45

Gly Ser Arg Ser Cys Gly Ile Val Glu Ser Arg Thr Arg Arg Gln
50 55 60

<210> SEQ ID NO 19

<211> LENGTH: 6624

<212> TYPE: DNA

<213> ORGANISM: mosquito baculovirus

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (4127)...(4735)

<221> NAME/KEY: CDS

<222> LOCATION: (1237)...(1809)

<221> NAME/KEY: CDS

<222> LOCATION: (2500)...(3021)

<221> NAME/KEY: CDS

<222> LOCATION: (4994)...(5344)

<221> NAME/KEY: CDS

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<222> LOCATION: (5401)...(5721)
<221> NAME/KEY: CDS
<222> LOCATION: (4740)...(4982)
<221> NAME/KEY: CDS
<222> LOCATION: (2)...(196)
<221> NAME/KEY: CDS
<222> LOCATION: (3790)...(3939)

<400> SEQUENCE: 19

a agc ttg gcg ccg tgc tgc aga ttc tac gat acc gca cga cct gga gcc      49
  Ser Leu Ala Pro Cys Ser Arg Phe Tyr Asp Thr Ala Arg Pro Gly Ala
    1           5            10          15

cga cga aat gtt ggc ccg ggt cga caa agt ccc cca gct gtc tgt tgc cca      97
  Arg Arg Asn Val Gly Pro Gly Arg Gln Ser Pro Pro Ala Val Cys Pro
    20          25            30

aat cgg cca tgg ttg agt gag ttg gtc ggt gaa agt ggg gtc ttg ctc      145
  Asn Arg Pro Trp Leu Ser Glu Leu Val Gly Ser Gly Val Leu Leu
    35          40            45

gat agg gtg gaa acg ttc ctc tat ccc gtc cag gtt acc agt gca caa      193
  Asp Arg Val Glu Thr Phe Leu Tyr Pro Val Gln Val Thr Ser Ala Gln
    50          55            60

gca tgagctcccg ggcgctacgg tcgagaatca ggaagtttag tttgtaaaca      246
  Ala
  65

agaagccggc ccttttgtgc ggcgcgcac agtcataaat cgaataccctt ttttatttat      306
  attattattt ttatttttgt tgttttttt tctttccagt tccaatatac ttggggaaaat      366
  aaaataaaaaa aaaaactcta tacacttgtt ggtttttatg tccctgtttt aagcgatttt      426
  ttttttatta taaagggtgt cgtaaatcac acccagggttg tttttcttcc acggtaaagt      486
  tgggctcagg gtggaccgcg aggtggtagc accactttagc catgtgcgtt gtcaccggc      546
  gtgctcaat tccaccgtaa aatatttcgc ccgcccagtt gagggtatag ttgcgtgtat      606
  cccactgcac gacgagcatc aaactgttgt ccagtgcggc ccacgggtt aatagaaaact      666
  ggcaccgcaa atcgcactg ggcgacacga gtgtgaagtg gggcctact agggaaaactt      726
  gtaacatcgt tgggttgcgg gcggttaac aatgaaagac ggggtgttta taattccaaa      786
  ctttgagatt tatttgcagt gaaatcgact tctatcgtgt acttcatagc ggcgtcaaac      846
  ttctcgatta tccttaacgc tagatcgta tactgcacgc ccggcagtt ctccaaactgg      906
  tactctagtg gtggatcgta cacatcccg cacttgttagg tggctctcg ccatacgcag      966
  gaaaatttt tactaccctt gacggtaaca cacaaccgtt tcgtgtggtc gagcggtata      1026
  tcgttccgtt aaatccatc gacggtccat ctatctt cgaacggat ggcgatatgg      1086
  tggggatgtt gcagcgactg cgacggaaatc tcgtactaa atacgcgaaat ttctacagag      1146
  tacaacattt tgcgtatact gctacgattt gtcgtgttgc atcgattttt agtacgatatt      1206
  tttaaagagt agctgaactt caccgcaaaat atg tac agc ttt tcg ggt aca ttt      1260
  Met Tyr Ser Phe Ser Gly Thr Phe
    70

gtg cac gtt gga gct gaa aat cgt cga acc atc ttt cgg tac ctg cgc      1308
  Val His Val Gly Ala Glu Asn Arg Arg Thr Ile Phe Arg Tyr Leu Arg
    75          80            85

cac ccg ttg acg aga ttt tta tac gtg gac cac cag ttg gcg gtg cgg      1356
  His Pro Leu Thr Arg Phe Leu Tyr Val Asp His Gln Leu Ala Val Arg
    90          95            100          105

ggc ttc gta cag tac gaa gcc tac aac ata aat agc agc ttt ggc aac      1404
  Gly Phe Val Gln Tyr Glu Ala Tyr Asn Ile Asn Ser Ser Phe Gly Asn
    110         115            120

gta acg gca gcg ggc cac gat ttg gcc cta atg tcg ccc gcc gag tgg      1452

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Val Thr Ala Ala Gly His Asp Leu Ala Leu Met Ser Pro Ala Glu Trp				
125	130	135		
gag tgg cac gaa aat acg gtc ctc atc acg ccg cac ggt tta ccg aaa				1500
Glu Trp His Glu Asn Thr Val Leu Ile Thr Pro His Gly Leu Pro Lys				
140	145	150		
atg atc ccc ttc gag ctg ccc caa gag ctg ctc gag tac gga gaa gtt				1548
Met Ile Pro Phe Glu Leu Pro Gln Glu Leu Leu Glu Tyr Gly Glu Val				
155	160	165		
acc tca ttg gca ccg gaa aag ttt ctt cta gtt tta cat tac gac atg				1596
Thr Ser Leu Ala Pro Glu Lys Phe Leu Leu Val Leu His Tyr Asp Met				
170	175	180	185	
gac ctg ccg tcc atc tcc atg cga gtg tgc gac ggt aca gaa gtg				1644
Asp Leu Arg Ser Ile Ser Met Arg Val Val Cys Asp Gly Thr Glu Val				
190	195	200		
atg tac gag agt cga gat ttg gag tac tac ttt ggc tac tgt tta aac				1692
Met Tyr Glu Ser Arg Asp Leu Glu Tyr Tyr Phe Gly Tyr Cys Leu Asn				
205	210	215		
atc gat gtg cgc tat cta agc gcg aag caa ctg ctg gac ctg gtc ggc				1740
Ile Asp Val Arg Tyr Leu Ser Ala Lys Gln Leu Leu Asp Leu Val Gly				
220	225	230		
aaa tgc ttc ccc gat gag ctg caa ttt atg gag ggt ttg gtg gag aaa				1788
Lys Cys Phe Pro Asp Glu Leu Gln Phe Met Glu Gly Leu Val Glu Lys				
235	240	245		
tcg agg gca gtt tta gaa aaa taaaacactt gatgatgtaa actaaaggta				1839
Ser Arg Ala Val Leu Glu Lys				
250	255			
tttgtttatt tctctccct ttcttccaag cgaaaaatgtt tgctcaacag ctccctaata				1899
caccctcttc atccaagccc gacttcatacg cagcctcggtt cagtagctca agccatagat				
cgatgtataatc cccactgggt gaactgtaaa gtttgcccc atcgattggc ctcagctgt				2019
cgaaaaatttc cggatggta agtgotataat agcgcataag gtggggtttcaaatcgacaa				2079
tacactggta caggcgggt tccacgttgg cctcgaaacc agcgacatag cacgacaatc				2139
cgcgcgttca aatgtgcacc aaggcatgg ttcaatgact ccacgggtct gcgggtataa				2199
ggatggattt gtagttcgat gatgcggact ggcgcgttgcgt gtttggccgt aataacgctc				2259
aatctaactg gttcacctc gacactttgc ctataaacgg ggaggttatg aatgtcgctc				2319
gtaaaaacga tcctctctta tggtagccca cagttcagga gaatttttat acctttcgac				2379
cgctcacggc gctgaaactg agagaaaaag gtcgcgttga cggattctat ccaccaacta				2439
cggaccactg gtttatcgag tcgagggtgt tcgcagccaa gttgttgaa tcgctgttca				2499
atg ctt gtc gcg tcg tat ccg cga gag gta ctg cgg gag caa att ata				
Met Leu Val Ala Ser Tyr Pro Arg Glu Val Leu Arg Glu Gln Ile Ile				
260	265	270		
cgc gcc gct agt gcc cac aac ttg gtg tta ctt tca tgc gac ccg gac				2595
Arg Ala Ala Ser Ala His Asn Leu Val Leu Ser Cys Asp Pro Asp				
275	280	285		
ctg gtt aac gag tgc aca aat ttg ctg gta gat ttg aaa ctt ttt agc				2643
Leu Val Asn Glu Cys Thr Asn Leu Leu Val Asp Leu Lys Leu Phe Ser				
290	295	300		
acc ata gtt gac gcc cga cgc ctg cac gaa act tgg atg gta ttg gtg				2691
Thr Ile Val Asp Ala Arg Arg Leu His Glu Thr Trp Met Val Leu Val				
305	310	315	320	
aat aac gtt agc caa tgt tgg tac cac tat act gga gac ttt ggc act				2739
Asn Asn Val Ser Gln Cys Trp Tyr His Tyr Thr Gly Asp Phe Gly Thr				
325	330	335		
gca att cgt cag ctc aac cat gtt acg gtc aac ggt ccg gtg gtc cta				2787
Ala Ile Arg Gln Leu Asn His Val Thr Val Asn Gly Pro Val Val Leu				

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340	345	350	
ttg ctc gat att aaa aat caa cgc gat ctt gca aag att ctg ctg gaa Leu Leu Asp Ile Lys Asn Gln Arg Asp Leu Ala Lys Ile Leu Leu Glu 355	360	365	2835
cat tat tgg gag gct cgt atg gtg gta ctg cac cga act gga cag gct His Tyr Trp Glu Ala Arg Met Val Val Leu His Arg Thr Gly Gln Ala 370	375	380	2883
tgc aac ttg ggt cac tgt gtg aac gtc gac cta aag agc ggc cag tgt Cys Asn Leu Gly His Cys Val Asn Val Asp Leu Lys Ser Gly Gln Cys 385	390	395	2931
gta cga ttc ggc ggt ggt cta tct gtg ata aac gca cca cac cgc gct Val Arg Phe Gly Gly Leu Ser Val Ile Asn Ala Pro His Arg Ala 405	410	415	2979
aat gtt gtg atg aaa aat gtg atc aaa tat aat aat acc tgt Asn Val Val Met Lys Asn Val Ile Lys Tyr Asn Asn Thr Cys 420	425	430	3021
tagagttaga aaatttttat ttttattcaa caaaaaccca acccccttag caccgcaat			3081
gtggggccca caaaagtggaa cccgtcttgg ttgggctaac ttttccatat ggagcccaac			3141
atttggcgcc cccacaaaaag tggacccgtt aaagtctgtc taacaaatga acattttca			3201
tttaatggag ccgcagtcgg ggttgaactt gtgatgttg gggataaaa aacttcaatg			3261
agtcatgtt aataaaaactt ttatattcaa tcattttaa aatattcatc caagtcaata			3321
cgacgcgaaa gccgaccgcc cttaaagtgg taactgaggg gtgcacggca gagtctagct			3381
ggcgattgaa acaggcccgc atctatggc gcacaaaaga gtctccacac gtcggtgacg			3441
gtgctcacca cgtcccggtt gttcgctata atcgatgtca tttcggtcat ataggttcg			3501
ttgcagcaga gagcgcgcac aaagcactcg gcaaacgaaa tcggttccgt gggattgggt			3561
gggggtgtcga tgatgcgcat ctggggctt caatcgattt cgcagcagtc ggcgtcgcaa			3621
aacaacctgc actcggttgtt ccgcaccaggc tcgtgttagtt ctccttcacc ttgggttagc			3681
tgcattggcgg cgaggtagaa tccgcgcata tcggcgcctcg agtccaccgg gaagttggcc			3741
gggtttagcc aaatgtggat gccgtcggtt cccgtgttgtt aaacttta atg ttt tcg Met Phe Ser			3798
gta ccg aag aac att gag gtg acc acg gac acg ttg agc aca aag Val Pro Lys Lys Asn Ile Glu Val Thr Thr Asp Thr Leu Ser Thr Lys 435	440	445	3846
ttg gcc aac tcg ggg tcg tca gtt ttc aaa tcg ata tca atc acc cac Leu Ala Asn Ser Gly Ser Ser Val Phe Lys Ser Ile Ser Ile Thr His 450	455	460	3894
465			
tct cgg cag ccc cgg ttc ccg cgg gtg tgc agc cca caa atg cca Ser Arg Gln Pro Arg Phe Pro Arg Val Cys Ser Pro Gln Met Pro 470	475	480	3939
tagctcgacc ggtatgggtc ggtttagt tagtacggtct cgatgaattc actcattgtg			3999
tcgaattctt ccgggtggcaa ccacaccctt tcgcttagct gaagggccca tttgcgtcc			4059
tcggggcttct cgaaagtgtt ccaaattgtt ttaagttggg attcctgtgg aaatagaaaag			4119
ggaagaa atg ttg tac ggt tta gtg gtg ctc ata ctg gtg ctc gta atg Met Leu Tyr Gly Leu Val Val Leu Ile Leu Val Leu Val Met 485	490		4168
att cag ttg att tta act tcg ggt gca aaa ttt cta gcc aaa cac gcc Ile Gln Leu Ile Leu Thr Ser Gly Ala Lys Phe Leu Ala Lys His Ala 495	500	505	4216
510			
caa gag tcg cgg gaa cgg gcc gca cga gct cgg ggt gaa tcg gtg ctg Gln Glu Ser Arg Glu Arg Ala Ala Arg Ala Arg Gly Glu Ser Val Leu 515	520	525	4264

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cca gag att cat ttc gcc ggc tct cag cac gta gat tgc cac aac acc Pro Glu Ile His Phe Ala Gly Ser Gln His Val Asp Cys His Asn Thr 530 535 540	4312
aaa tta ccg tgt att gat aat gcg gac tgt caa cgt aac tgc gct ttg Lys Leu Pro Cys Ile Asp Asn Ala Asp Cys Gln Arg Asn Cys Ala Leu 545 550 555	4360
acc aga gac gga gga gtt tca tcg tgc ata ggc ggg ttc tgc agc acg Thr Arg Asp Gly Gly Val Ser Ser Cys Ile Gly Gly Phe Cys Ser Thr 560 565 570	4408
gat cat aaa tct att ccc gag aag cga aat tgt gtc gaa gag cat gga Asp His Lys Ser Ile Pro Glu Lys Arg Asn Cys Val Glu Glu His Gly 575 580 585 590	4456
att tta ccg gta ttc act gca gac gaa ttc gtt ata aat caa tcc tgc Ile Leu Arg Val Phe Thr Ala Asp Glu Phe Val Ile Asn Gln Ser Cys 595 600 605	4504
ctt tca acc tat ccg gac att ttc acc gac gat aac aaa ctg caa ccg Leu Ser Thr Tyr Arg Asp Ile Phe Thr Asp Asp Asn Lys Leu Gln Pro 610 615 620	4552
tat gtg tgt acc ggc ggt caa ttg gag ata aac ttg ctc gag caa gcg Tyr Val Cys Thr Gly Gly Gln Leu Glu Ile Asn Leu Glu Gln Ala 625 630 635	4600
ttc act ccg gac gct tgt gtg tgc ggg act ggt aca acg aaa tac att Phe Thr Pro Asp Ala Cys Val Cys Gly Thr Gly Thr Thr Lys Tyr Ile 640 645 650	4648
tac ccg ccg ggg ccg tat aat ccg ccc att ccg gtg tgc ttg acc aag Tyr Arg Pro Gly Pro Tyr Asn Arg Pro Ile Pro Val Cys Leu Thr Lys 655 660 665 670	4696
cag caa gct gcg ctc cta gga cga gtt tac gag cgg gcg taaa atg tgt Gln Gln Ala Ala Leu Leu Gly Arg Val Tyr Glu Arg Ala Met Cys 675 680 685	4745
cga gtc tcg gtt gat att gtg gtg cgg aac ctg cgc aaa cgg cgc ttc Arg Val Ser Val Asp Ile Val Val Arg Asn Leu Arg Lys Arg Arg Phe 690 695 700	4793
tac ccg ccg aat ttt gtg cta cca gag ggg cac acg gag atc agt tat Tyr Arg Arg Asn Phe Val Leu Pro Glu Gly His Ser Glu Ile Ser Tyr 705 710 715	4841
atg ggt gcc tgt gag tac gga gtg tat ttg gtg tca cga acg ggc cgg Met Gly Ala Cys Glu Tyr Gly Val Tyr Leu Val Ser Arg Thr Gly Arg 720 725 730	4889
gcg gtg gtg acc gtt gac ggc cgg tta ctc gag gac acc ctg gag ggt Ala Val Val Thr Val Asp Gly Arg Leu Leu Glu Asp Thr Leu Glu Gly 735 740 745	4937
ttc ggt ccg ctg cgg ttg gtc tca cgg tgc acc tgt tcc ccg cca Phe Gly Pro Leu Arg Leu Val Ser Arg Cys Thr Cys Ser Pro Pro 750 755 760	4982
taaggctcac g atg tcg tca ccc ctt gta ata ttt tta att ttt ata ctg Met Ser Ser Pro Leu Val Ile Phe Leu Ile Phe Ile Leu 765 770 775	5032
aca atg tta acg ata atg acc gcg atc aca atc ttc acc gtc aag ggt Thr Met Leu Thr Ile Met Thr Ala Ile Thr Ile Phe Thr Val Lys Gly 780 785 790	5080
gcc aag cgt gaa tgt ggg gac gac cat ttg ccg gac ctg tcc cca ttg Ala Lys Arg Glu Cys Gly Asp Asp His Leu Pro Asp Leu Ser Pro Leu 795 800 805	5128
aag gag ccg gtt acc gcc acg gag caa cag ttg acg gac acg gag cag Lys Glu Arg Val Thr Ala Thr Glu Gln Gln Leu Ser Asp Thr Glu Gln 810 815 820 825	5176
cgc att gac gag gtc gaa cgg tcg ggt gtg gaa aat ttt acg gca atc Arg Ile Asp Glu Val Glu Arg Ser Gly Val Glu Asn Phe Ser Ala Ile 830 835 840	5224

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ggc gaa aca ttg gag aat ata tcg ggc gag ctg gtg gag ctg caa aac Gly Glu Thr Leu Glu Asn Ile Ser Gly Glu Leu Val Glu Leu Gln Asn 845 850 855	5272
tcg acc tcg tca aag ttt tac gaa att ggc aac gag ctg gtg aac ctg Ser Thr Ser Ser Lys Phe Tyr Glu Ile Gly Asn Glu Leu Val Asn Leu 860 865 870	5320
gat ctg cgc gtc cag tcg cta gag tgagtgccga aattcagtagtac cagtgggttg Asp Leu Arg Val Gln Ser Leu Glu 875 880	5374
acggtagctg caagtaagag ccaacg atg ccc caa act tta cta ttt cta att Met Pro Gln Thr Leu Leu Phe Leu Ile 885 890	5427
cta cta cta ctg gtc aca atg gtg gcc gtg ctc atc atg cgc tac cca Leu Leu Leu Val Thr Met Val Ala Val Leu Ile Met Arg Tyr Pro 895 900 905	5475
gcc caa cct ccc gag tgc aag tgc gag gag ggc tcg ggg gtg gac ctc Ala Gln Pro Pro Glu Cys Lys Cys Glu Glu Ser Gly Val Asp Leu 910 915 920	5523
acc aaa ctc acg gct aga gtg gac gag ctc gag caa aag ctt ggc ccc Thr Lys Leu Thr Ala Arg Val Asp Glu Leu Glu Gln Lys Leu Gly Pro 925 930 935	5571
atg aac acc acc ttg ggc aaa ctg aac gac gac ctg tcg gag ctg tcc Met Asn Thr Thr Leu Gly Lys Leu Asn Asp Asp Leu Ser Glu Leu Ser 940 945 950	5619
agc tcc agt gat gat aaa ttt tca tac ata aac gtc gcc atc aat gag Ser Ser Ser Asp Asp Lys Phe Ser Tyr Ile Asn Val Ala Ile Asn Glu 955 960 965 970	5667
ctg gcc gac agt atc aaa acg atg gac caa cgc ttg aag gtg ctg gag Leu Ala Asp Ser Ile Lys Thr Met Asp Gln Arg Leu Lys Val Leu Glu 975 980 985	5715
gga gag tgatatattt actgctcaa taaaacgagg tgtataaatt ttatcatttt Gly Glu	5771
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cagttccgac cgagttgggtt gtcgtgcactt attacccaa cacttgtacg ttttgtccag	6251
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tcgattcatg ctgcttagttt ccagccgagc cccgaaacca accttttatat accccgttat	6611
catgagagaa ttc	6624

<210> SEQ ID NO 20

<211> LENGTH: 65

<212> TYPE: PRT

<213> ORGANISM: mosquito baculovirus

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<400> SEQUENCE: 20

Ser Leu Ala Pro Cys Ser Arg Phe Tyr Asp Thr Ala Arg Pro Gly Ala
1 5 10 15

Arg Arg Asn Val Gly Pro Gly Arg Gln Ser Pro Pro Ala Val Cys Pro
20 25 30

Asn Arg Pro Trp Leu Ser Glu Leu Val Gly Glu Ser Gly Val Leu Leu
35 40 45

Asp Arg Val Glu Thr Phe Leu Tyr Pro Val Gln Val Thr Ser Ala Gln
50 55 60

Ala
65

<210> SEQ ID NO 21

<211> LENGTH: 191

<212> TYPE: PRT

<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 21

Met Tyr Ser Phe Ser Gly Thr Phe Val His Val Gly Ala Glu Asn Arg
1 5 10 15

Arg Thr Ile Phe Arg Tyr Leu Arg His Pro Leu Thr Arg Phe Leu Tyr
20 25 30

Val Asp His Gln Leu Ala Val Arg Gly Phe Val Gln Tyr Glu Ala Tyr
35 40 45

Asn Ile Asn Ser Ser Phe Gly Asn Val Thr Ala Ala Gly His Asp Leu
50 55 60

Ala Leu Met Ser Pro Ala Glu Trp Glu Trp His Glu Asn Thr Val Leu
65 70 75 80

Ile Thr Pro His Gly Leu Pro Lys Met Ile Pro Phe Glu Leu Pro Gln
85 90 95

Glu Leu Leu Glu Tyr Gly Glu Val Thr Ser Leu Ala Pro Glu Lys Phe
100 105 110

Leu Leu Val Leu His Tyr Asp Met Asp Leu Arg Ser Ile Ser Met Arg
115 120 125

Val Val Cys Asp Gly Thr Glu Val Met Tyr Glu Ser Arg Asp Leu Glu
130 135 140

Tyr Tyr Phe Gly Tyr Cys Leu Asn Ile Asp Val Arg Tyr Leu Ser Ala
145 150 155 160

Lys Gln Leu Leu Asp Leu Val Gly Lys Cys Phe Pro Asp Glu Leu Gln
165 170 175

Phe Met Glu Gly Leu Val Glu Lys Ser Arg Ala Val Leu Glu Lys
180 185 190

<210> SEQ ID NO 22

<211> LENGTH: 174

<212> TYPE: PRT

<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 22

Met Leu Val Ala Ser Tyr Pro Arg Glu Val Leu Arg Glu Gln Ile Ile
1 5 10 15

Arg Ala Ala Ser Ala His Asn Leu Val Leu Leu Ser Cys Asp Pro Asp
20 25 30

Leu Val Asn Glu Cys Thr Asn Leu Leu Val Asp Leu Lys Leu Phe Ser
35 40 45

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Thr Ile Val Asp Ala Arg Arg Leu His Glu Thr Trp Met Val Leu Val
 50 55 60
 Asn Asn Val Ser Gln Cys Trp Tyr His Tyr Thr Gly Asp Phe Gly Thr
 65 70 75 80
 Ala Ile Arg Gln Leu Asn His Val Thr Val Asn Gly Pro Val Val Leu
 85 90 95
 Leu Leu Asp Ile Lys Asn Gln Arg Asp Leu Ala Lys Ile Leu Leu Glu
 100 105 110
 His Tyr Trp Glu Ala Arg Met Val Val Leu His Arg Thr Gly Gln Ala
 115 120 125
 Cys Asn Leu Gly His Cys Val Asn Val Asp Leu Lys Ser Gly Gln Cys
 130 135 140
 Val Arg Phe Gly Gly Leu Ser Val Ile Asn Ala Pro His Arg Ala
 145 150 155 160
 Asn Val Val Met Lys Asn Val Ile Lys Tyr Asn Asn Thr Cys
 165 170

<210> SEQ ID NO 23
 <211> LENGTH: 50
 <212> TYPE: PRT
 <213> ORGANISM: mosquito baculovirus
 <400> SEQUENCE: 23

Met Phe Ser Val Pro Lys Lys Asn Ile Glu Val Thr Thr Asp Thr Leu
 1 5 10 15
 Ser Thr Lys Leu Ala Asn Ser Gly Ser Ser Val Phe Lys Ser Ile Ser
 20 25 30
 Ile Thr His Ser Arg Gln Pro Arg Phe Pro Arg Val Cys Ser Pro Gln
 35 40 45
 Met Pro
 50

<210> SEQ ID NO 24
 <211> LENGTH: 203
 <212> TYPE: PRT
 <213> ORGANISM: mosquito baculovirus
 <400> SEQUENCE: 24

Met Leu Tyr Gly Leu Val Val Leu Ile Leu Val Leu Val Met Ile Gln
 1 5 10 15
 Leu Ile Leu Thr Ser Gly Ala Lys Phe Leu Ala Lys His Ala Gln Glu
 20 25 30
 Ser Arg Glu Arg Ala Ala Arg Ala Arg Gly Glu Ser Val Leu Pro Glu
 35 40 45
 Ile His Phe Ala Gly Ser Gln His Val Asp Cys His Asn Thr Lys Leu
 50 55 60
 Pro Cys Ile Asp Asn Ala Asp Cys Gln Arg Asn Cys Ala Leu Thr Arg
 65 70 75 80
 Asp Gly Gly Val Ser Ser Cys Ile Gly Gly Phe Cys Ser Thr Asp His
 85 90 95
 Lys Ser Ile Pro Glu Lys Arg Asn Cys Val Glu Glu His Gly Ile Leu
 100 105 110
 Arg Val Phe Thr Ala Asp Glu Phe Val Ile Asn Gln Ser Cys Leu Ser
 115 120 125
 Thr Tyr Arg Asp Ile Phe Thr Asp Asp Asn Lys Leu Gln Pro Tyr Val
 130 135 140

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Cys Thr Gly Gly Gln Leu Glu Ile Asn Leu Leu Glu Gln Ala Phe Thr
145 150 155 160

Pro Asp Ala Cys Val Cys Gly Thr Gly Thr Thr Lys Tyr Ile Tyr Arg
165 170 175

Pro Gly Pro Tyr Asn Arg Pro Ile Pro Val Cys Leu Thr Lys Gln Gln
180 185 190

Ala Ala Leu Leu Gly Arg Val Tyr Glu Arg Ala
195 200

<210> SEQ ID NO 25
<211> LENGTH: 81
<212> TYPE: PRT
<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 25

Met Cys Arg Val Ser Val Asp Ile Val Val Arg Asn Leu Arg Lys Arg
1 5 10 15

Arg Phe Tyr Arg Arg Asn Phe Val Leu Pro Glu Gly His Ser Glu Ile
20 25 30

Ser Tyr Met Gly Ala Cys Glu Tyr Gly Val Tyr Leu Val Ser Arg Thr
35 40 45

Gly Arg Ala Val Val Thr Val Asp Gly Arg Leu Leu Glu Asp Thr Leu
50 55 60

Glu Gly Phe Gly Pro Leu Arg Leu Val Ser Arg Cys Thr Cys Ser Pro
65 70 75 80

Pro

<210> SEQ ID NO 26
<211> LENGTH: 117
<212> TYPE: PRT
<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 26

Met Ser Ser Pro Leu Val Ile Phe Leu Ile Phe Ile Leu Thr Met Leu
1 5 10 15

Thr Ile Met Thr Ala Ile Thr Ile Phe Thr Val Lys Gly Ala Lys Arg
20 25 30

Glu Cys Gly Asp Asp His Leu Pro Asp Leu Ser Pro Leu Lys Glu Arg
35 40 45

Val Thr Ala Thr Glu Gln Gln Leu Ser Asp Thr Glu Gln Arg Ile Asp
50 55 60

Glu Val Glu Arg Ser Gly Val Glu Asn Phe Ser Ala Ile Gly Glu Thr
65 70 75 80

Leu Glu Asn Ile Ser Gly Glu Leu Val Glu Leu Gln Asn Ser Thr Ser
85 90 95

Ser Lys Phe Tyr Glu Ile Gly Asn Glu Leu Val Asn Leu Asp Leu Arg
100 105 110

Val Gln Ser Leu Glu
115

<210> SEQ ID NO 27
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 27

Met Pro Gln Thr Leu Leu Phe Leu Ile Leu Leu Leu Val Thr Met
1 5 10 15

-continued

Val Ala Val Leu Ile Met Arg Tyr Pro Ala Gln Pro Pro Glu Cys Lys
20 25 30

Cys Glu Glu Gly Ser Gly Val Asp Leu Thr Lys Leu Thr Ala Arg Val
35 40 45

Asp Glu Leu Glu Gln Lys Leu Gly Pro Met Asn Thr Thr Leu Gly Lys
50 55 60

Leu Asn Asp Asp Leu Ser Glu Leu Ser Ser Ser Asp Asp Lys Phe
65 70 75 80

Ser Tyr Ile Asn Val Ala Ile Asn Glu Leu Ala Asp Ser Ile Lys Thr
85 90 95

Met Asp Gln Arg Leu Lys Val Leu Glu Gly Glu
100 105

<210> SEQ ID NO 28
<211> LENGTH: 6624
<212> TYPE: DNA
<213> ORGANISM: mosquito baculovirus
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1444)...(1788)
<221> NAME/KEY: CDS
<222> LOCATION: (3977)...(4285)
<221> NAME/KEY: CDS
<222> LOCATION: (965)...(1153)
<221> NAME/KEY: CDS
<222> LOCATION: (534)...(857)

<400> SEQUENCE: 28

gaatttctc atgataacgg ggttatataaa ggttggtttc ggggctcgcc tggAACCTAG	60
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ggttcaactgc gaacagagac tggaagcggtt agaccgcgt gtggacgcgg aaacggagg	180
tatttatctt gggcttagtg tgcgcaatcg ttacagtcat cgggtggttt accgggcattg	240
gtcgcgacgtt ggggtcgcgc agcggaaactg gtttgtgaa attgaattac cacaagcggt	300
gctcgacgct aaccattaca ttttaattta ttccggcaca cggatctatt gccaacagcc	360
gtggctaacg tacctggaca aaacgtacaa gtgttgggtt aatagtgcac gacaaccaac	420
tcgggtcgaa ctgaagcgcg tacctagcac ctactggcgc cacaacacca cctatataac	480
gatggacgcg cgatcatttc gaccacttgt ccgcttcatg atcgacgtcc acg atg	536
Met 1	
aac gct gac tgt ttc tgc cca ccc gga ccc tgc tac cat gca ctc ttc	584
Asn Ala Asp Cys Phe Cys Pro Pro Gly Pro Cys Tyr His Ala Leu Phe	
5 10 15	
agc cac tgc gga ggt atc tgc cag tcc tgt gga acc cac tac gaa gac	632
Ser His Cys Gly Gly Ile Cys Gln Ser Cys Gly Thr His Tyr Glu Asp	
20 25 30	
cta gac gag ttc gtg cgc tgt atg agg ggc cag acc acc cac aaa ccg	680
Leu Asp Glu Phe Val Arg Cys Met Arg Gly Gln Thr Thr His Lys Pro	
35 40 45	
aac ccc atc gcc ata aca atg ggg ctc tgc gaa tac tgt ccg aga agg	728
Asn Pro Ile Ala Ile Thr Met Gly Leu Cys Glu Tyr Cys Pro Arg Arg	
50 55 60 65	
cac ccg gtc ggc gtg tcc tgc caa ggc tat cca gcg tgc gaa aaa tgt	776
His Pro Val Gly Val Ser Cys Gln Gly Tyr Pro Ala Cys Glu Lys Cys	
70 75 80	
tcc ctg tcg cac gcc cca ctc ccc caa tgt ccc cac cga tta agc cta	824
Ser Leu Ser His Ala Pro Leu Pro Gln Cys Pro His Arg Leu Ser Leu	
85 90 95	

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tat ttc ttt ctt ttc aag aaa aat aat aaa aaa tgataaaaatt tatacacccctc Tyr Phe Leu Phe Lys Lys Asn Asn Lys Lys 100 105	877
gttttattgc agcagtaaat atatcaactc ccctccagca ccttcaagcg ttggccatc gttttgatac tgtcgccag ctcattg atg gcg acg ttt atg tat gaa aat tta Met Ala Thr Phe Met Tyr Glu Asn Leu 110 115	937 991
tca tca ctg gag ctg gac agc tcc gac agg tcg tcg ttc agt ttg ccc Ser Ser Leu Glu Leu Asp Ser Ser Asp Arg Ser Ser Phe Ser Leu Pro 120 125 130	1039
aag gtg gtg ttc atg ggg cca agc ttt tgc tcg agc tcg tcc act cta Lys Val Val Phe Met Gly Pro Ser Phe Cys Ser Ser Ser Thr Leu 135 140 145	1087
gcc gtg agt ttg gtg agg tcc acc ccc gag ccc tcc tcg cac ttg cac Ala Val Ser Leu Val Arg Ser Thr Pro Glu Pro Ser Ser His Leu His 150 155 160 165	1135
tcg gga ggt tgg gct ggg tagcgcata tgagcgcac caccattgtg Ser Gly Gly Trp Ala Gly 170	1183
accagtagta gtagaattag aaatagtaaa gttggggca tcgttggctc ttacttgcag ctaccgtcaa accactggta ctgaatttcg gcactcaactc tagcgactgg acgcgcagat ccaggttac cagctcggt ccaatttcgt aaaactttga cgaggtcgag ttttgcagct ccaccagctc gcccataata ttctccaatg ttccgcgtat tgcgctaaaa ttttccacac ccgaccgttc gacctcgatc atg cgc tgc tcc gtg tcg ctc aac tgt tgc tcc Met Arg Cys Ser Val Ser Leu Asn Cys Cys Ser 175 180	1243 1303 1363 1423 1476
gtg gcg gta acg cgc tcc ttc aat ggg gac agg tcc ggc aaa tgg tcg Val Ala Val Thr Arg Ser Phe Asn Gly Asp Arg Ser Gly Lys Trp Ser 185 190 195	1524
tcc cca cat tca cgc ttg gca ccc ttg acg gtg aag att gtg atc gcg Ser Pro His Ser Arg Leu Ala Pro Leu Thr Val Lys Ile Val Ile Ala 200 205 210	1572
gtc att atc gtt aac att gtc agt ata aaa att aaa aat att aca agg Val Ile Ile Val Asn Ile Val Ser Ile Lys Ile Lys Asn Ile Thr Arg 215 220 225 230	1620
ggt gac gac atc gtg agg ctt atg gcg ggg aac agg tgc acc gtg aga Gly Asp Asp Ile Val Arg Leu Met Ala Gly Asn Arg Cys Thr Val Arg 235 240 245	1668
cca acc gca gcg gac cga aac cct cca ggg tgt cct cga gta acc ggc Pro Thr Ala Ala Asp Arg Asn Pro Pro Gly Cys Pro Arg Val Thr Gly 250 255 260	1716
cgt caa cgg tca cca ccg ccc ggc ccg ttc gtg aca cca aat aca ctc Arg Gln Arg Ser Pro Pro Gly Pro Phe Val Thr Pro Asn Thr Leu 265 270 275	1764
cgt act cac agg cac cca tat aac tgatctcgct gtgccccctct ggttagcaca Arg Thr His Arg His Pro Tyr Asn 280 285	1818
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atacacggta atttggtgtt gtggaatct acgtgctgag agccggcgaa atgaatctct	2358
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ggtgtgtttg ccacccggAA aattcgacac aatgtgtgaa ttcatcgaga ccgtacacta	2658
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ctgcggAAAtC gattgcaAGC ccaagatGCG catcatcgAC acccccacCCA atccccacGGa	3078
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cgaaatgACA tcgattatac gcaacaACG ggacgtggTG agcaccGTCA ccgacgtGTG	3198
gagactctt ttggcccccA tagatgcGGG cctgtttCAA tcGCCAGCTA gactctGCCG	3258
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atatttAAAtA aatgattgAA ataaaaAGTT ttatTAACAA tgactcATTG aagtttttat	3378
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gaaaAGttag cccaaCCAAAG acgggtccAC ttttggggGG cccacatttG cggtgctAA	3558
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aatcttgcA agatcgcGTT gatTTtaAT atcgaGcaAT agcaccACCG gaccgttGAC	3858
cgtAACatGG ttgagctgAC gaatttgcAGT gccaaAGtCT ccagtataAGT ggtaccaACa	3918
ttggctAACG ttattcacCA ataccatCCA agtttgcgtc aggCGTCGGG cgtcaact	3976
atG gtG cta AAA AGt ttc AAA tct ACC AGC AAA ttt GTG CAC TCG tta Met Val Leu Lys Ser Phe Lys Ser Thr Ser Lys Phe Val His Ser Leu	4024
290 295 300	
acc agg tcc ggg tcg cat gaa agt aac acc aag ttg tgg gca cta gcg Thr Arg Ser Gly Ser His Glu Ser Asn Thr Lys Leu Trp Ala Leu Ala	4072
305 310 315	
gCG cgt ATA ATT tgc tcc CGC AGT ACC TCT CGC GGA TAC GAC GCG ACA Ala Arg Ile Ile Cys Ser Arg Ser Thr Ser Arg Gly Tyr Asp Ala Thr	4120
320 325 330	
agc ATT gAA cAG cGA ttc cAA cAA ctt ggc tgc gAA gCA CCT CGA CTC Ser Ile Glu Gln Arg Phe Gln Leu Gly Cys Glu Ala Pro Arg Leu	4168
335 340 345 350	
gat AAC cCA gTG gTC cgt AGT tgg tgg ATA gAA tCC gTC AAA gCG ACC Asp Asn Pro Val Val Arg Ser Trp Trp Ile Glu Ser Val Lys Ala Thr	4216
355 360 365	

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ttt ttc tct cag ttc cag cgc cgt gag cgg tcg aaa ggt ata aaa att	4264
Phe Phe Ser Gln Phe Gln Arg Arg Glu Arg Ser Lys Gly Ile Lys Ile	
370 375 380	
ctc ctg aac tgt ggc gta cca taagagagga tcgttttac gagcgacatt	4315
Leu Leu Asn Cys Gly Val Pro	
385	
cataaacctcc ccgttatag gcaaagtgtc gaggtgaaac cagtttagatt gagcgttatt	4375
acggccaaac acgaccgcgc agtccgcate acgaacatac aaatccatcc ttatcaccgc	4435
agaccggtgg agtcattgaa ccatgccctt ggtgcacatt gaacagcgcg gattgtcgtg	4495
ctatgtcgct ggtttcgagg ccaacgtgga acccgacctg taccagtgtt ttgtcgattt	4555
caaaccac cttatgcgct atatagcact taaccatccg gaattttcg cacagctgag	4615
gccaatcgat gggcacaacc tttagtgc caccagtggg gattacatcg atctatggct	4675
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ataaaattgca gctcatcggg gaagcatttg ccgaccaggc ccagcgttgc ttgcgcgtt	4915
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gccaacttgtt ggtccacgtt taaaatctc gtcaacgggtt ggccgcaggta cccggaaatgt	5335
gttcgacgtt tttcagctcc aacgtgcaca aatgtacccg aaaagctgtt catgtttcg	5395
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ctagcgtaa ggataatcgta gaagtttgcg cgcgcgtatgtt agtacacgtt agaagtcgtt	5815
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cctcgccgttcc accctgttgc ccaacttttac cgtggaaagaa aaacaacactt gtcgttgcgtt	6175
acgacaccctt ttataataaaa aaaaaatcg cttcaaacag ggacaataaaa acccacaagt	6235
gtatagagttt ttttttttcc caagtatattt ggaactggaa agaaataataa	6295
acaacaataa taacaataat aatatacaata aaaaaggat ttcgttgcgtt actgttgcgtt	6355
cgcgcacaac agggccggct tcttgcgttcc accctgttgc cttcaaacag ggacaataaaa acccacaagt	6415

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gccccggagc tcatgcttgt gcactggtaa cctgcacggg atagaggaac gtttccaccc	6475
tatcgagcaa caccccaact tcaccgacca actcactcaa ccatggccga tttggacaca	6535
cagctggggg actttgtcga cccggccaa catttcgtcg ggctccaggt cgtgcggtat	6595
cgtagaatct cgaacacggc gccaagctt	6624

<210> SEQ ID NO 29
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 29

Met Asn Ala Asp Cys Phe Cys Pro Pro Gly Pro Cys Tyr His Ala Leu			
1	5	10	15
Phe Ser His Cys Gly Gly Ile Cys Gln Ser Cys Gly Thr His Tyr Glu			
20	25	30	
Asp Leu Asp Glu Phe Val Arg Cys Met Arg Gly Gln Thr Thr His Lys			
35	40	45	
Pro Asn Pro Ile Ala Ile Thr Met Gly Leu Cys Glu Tyr Cys Pro Arg			
50	55	60	
Arg His Pro Val Gly Val Ser Cys Gln Gly Tyr Pro Ala Cys Glu Lys			
65	70	75	80
Cys Ser Leu Ser His Ala Pro Leu Pro Gln Cys Pro His Arg Leu Ser			
85	90	95	
Leu Tyr Phe Phe Leu Phe Lys Lys Asn Asn Lys Lys			
100	105		

<210> SEQ ID NO 30
<211> LENGTH: 63
<212> TYPE: PRT
<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 30

Met Ala Thr Phe Met Tyr Glu Asn Leu Ser Ser Leu Glu Leu Asp Ser			
1	5	10	15
Ser Asp Arg Ser Ser Phe Ser Leu Pro Lys Val Val Phe Met Gly Pro			
20	25	30	
Ser Phe Cys Ser Ser Ser Ser Thr Leu Ala Val Ser Leu Val Arg Ser			
35	40	45	
Thr Pro Glu Pro Ser Ser His Leu His Ser Gly Gly Trp Ala Gly			
50	55	60	

<210> SEQ ID NO 31
<211> LENGTH: 115
<212> TYPE: PRT
<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 31

Met Arg Cys Ser Val Ser Leu Asn Cys Cys Ser Val Ala Val Thr Arg			
1	5	10	15
Ser Phe Asn Gly Asp Arg Ser Gly Lys Trp Ser Ser Pro His Ser Arg			
20	25	30	
Leu Ala Pro Leu Thr Val Lys Ile Val Ile Ala Val Ile Ile Val Asn			
35	40	45	
Ile Val Ser Ile Lys Ile Lys Asn Ile Thr Arg Gly Asp Asp Ile Val			
50	55	60	
Arg Leu Met Ala Gly Asn Arg Cys Thr Val Arg Pro Thr Ala Ala Asp			
65	70	75	80

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Arg Asn Pro Pro Gly Cys Pro Arg Val Thr Gly Arg Gln Arg Ser Pro
85 90 95

Pro Pro Gly Pro Phe Val Thr Pro Asn Thr Leu Arg Thr His Arg His
100 105 110

Pro Tyr Asn
115

<210> SEQ ID NO 32
<211> LENGTH: 103
<212> TYPE: PRT
<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 32

Met Val Leu Lys Ser Phe Lys Ser Thr Ser Lys Phe Val His Ser Leu
1 5 10 15

Thr Arg Ser Gly Ser His Glu Ser Asn Thr Lys Leu Trp Ala Leu Ala
20 25 30

Ala Arg Ile Ile Cys Ser Arg Ser Thr Ser Arg Gly Tyr Asp Ala Thr
35 40 45

Ser Ile Glu Gln Arg Phe Gln Gln Leu Gly Cys Glu Ala Pro Arg Leu
50 55 60

Asp Asn Pro Val Val Arg Ser Trp Trp Ile Glu Ser Val Lys Ala Thr
65 70 75 80

Phe Phe Ser Gln Phe Gln Arg Arg Glu Arg Ser Lys Gly Ile Lys Ile
85 90 95

Leu Leu Asn Cys Gly Val Pro
100

<210> SEQ ID NO 33
<211> LENGTH: 6624
<212> TYPE: DNA
<213> ORGANISM: mosquito baculovirus
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (2202)...(2555)
<221> NAME/KEY: CDS
<222> LOCATION: (4084)...(4251)

<400> SEQUENCE: 33

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tggcccggt cgacaaagtc cccagctgt gtgtccaaat cggccatggc tgagtggatt	120
ggtcggtgaa agtggggtgt tgctcgatag ggtggaaacg ttccctatac ccgtgcagg	180
taccagtgc caagcatgag ctccccggcg ctacggcga gaatcaggaa gttgagttt	240
taaacaagaa gccggccctg ttgtgcgcgc gcgcacagtc ataaatcgaa taccttttt	300
attgatatta ttattgttat tatgtttgtt attatttctt tccagttcca atatacttgg	360
aaaaataaaa taaaaaaaaaa actctataca cttgtgggtt ttattgtccc tggttgaagc	420
gattttttt ttattataaa ggggtcgta aatcacagcc aggttggttt tcttccacgg	480
taaagtggg ctcagggtgg accgcgaggt ggttagcacca cttgagcatg tgccgtgtca	540
ccggcgtgc tgcaattcca ccgtaaaata ttgcggccgc ccagttgagg gtatagttgc	600
gctgatccca ctgcacgacg agcatcaaac tttgtccag tgccggccac ggtggtaata	660
gaaactggca ccgcaaatcg ccactggcga gcacgagtgt gaagtgggtt cctactaggg	720
aaacttgtaa catcggtggg ttgcggggcgg gttacaatg aaagacgggtt gggttataat	780
tccaaacttt gagatttatt tgcagtgaaa tcgacttcta tcgtgtactt catagcgcgc	840

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tc当地	cgattatcct taacgctaga tcgctatact gcacccccc cagtttctcc aactggtaact cttagtgggtt atcgtaacaca tttccgcact tgtaggttgtt ctctcgccat acgcaggaaa attttttact acccctgac gtaaacacaca accgtatcgt gtggcgac ggtatatcgt tcggtaaaat gccatcgac gttccatctat ctttatcgaa cggtatggcg atatggtggg agtggtgca gcaactgcac ggaatctccg tactaaatac gcaacttct acagagtaca acattgtgt aatactgta cgattggta gcgtgaatcg attttagta cgatattta aagagtagct gaacttcacc gcaaacatgtt acagctttc gggtacattt gtgcacgtt gagctgaaaa tcgtcgaacc atcttcggt acctgcgcca cccgttgac agattttat acgtggacca ccagttggcg gtgcgggct tcgtacagta cgaaggctac aacataaata gcagtttgg caacgtaacg gcagcggggc acgatttgc cctaattgtcg cccgccgagt gggagtgcca cggaaatacgtt gtcctcatca cggccacgg tttaccgaaa atgatccccct tcgagctgcc ccaagagctg ctggagtagc gagaagttac ctcattggca ccggaaaagt ttcttcttagt ttacattac gacatggacc tgcggccat ctccatgcga gtgggtgc acggtagaca agttagtgc gagagtcgag atttggagta ctacttgc tactgtttaa acatcgatgt gcgttatcta agcgcgaagc aactgctgga cctggcgcc aaatgcttcc ccgatgagct gcaattttagt gagggtttgg tggagaaatc gaggcgatgtt ttagaaaaat aaaacacttg atgatgtaaa ctaaagttgtt ttgttttattt ctcttccctt tcttccaagg gaaaatgttt gctcaacacgc tccctaatcc accctttca tccaaaggccc acttcatagc agccctcggtt agtagctaa gcccataatc gatgtatcc ccactgggtt aactgtaaag gttgtgccc tcgattggcc tcagctgtgc gaaaattcc ggatggtaa gtgctatata ggcataagg tgggttttc aatcgacat acactggtagt acggcgggtt ccacggttgc ctcgaaacca ggcacatagc acgacaatcc ggcgtgttca atgtgcacca agggcatggt tcaatgactc caccgggtctg cggtgataag g atg gat ttg tat gtt Met Asp Leu Tyr Val 1 5	900 960 1020 1140 1200 1260 1320 1380 1440 1500 1560 1620 1680 1740 1800 1860 1920 1980 2040 2100 2160 2216 2264 2312 2360 2408 2456 2504 2552 2605
cgt gat gcg gac tgc gcg gtc gtg ttt ggc cgt aat aac gct caa tct Arg Asp Ala Asp Cys Ala Val Val Phe Gly Arg Asn Asn Ala Gln Ser 10 15 20	2264	
aac tgg ttt cac ctc gac act ttg cct ata aac ggg gag gtt atg aat Asn Trp Phe His Leu Asp Thr Leu Pro Ile Asn Gly Glu Val Met Asn 25 30 35	2312	
gtc gct cgt aaa aac gat cct ctc tta tgg tac gcc aca gtt cag gag Val Ala Arg Lys Asn Asp Pro Leu Leu Trp Tyr Ala Thr Val Gln Glu 40 45 50	2360	
aat ttt tat acc ttt cga ccg ctc acg gcg ctg gaa ctg aga gaa aaa Asn Phe Tyr Thr Phe Arg Pro Leu Thr Ala Leu Glu Leu Arg Glu Lys 55 60 65	2408	
ggt cgc ttt gac gga ttc tat cca cca act acg gac cac tgg gtt atc Gly Arg Phe Asp Gly Phe Tyr Pro Pro Thr Thr Asp His Trp Val Ile 70 75 80 85	2456	
gag tcg agg tgc ttc gca gcc aag ttg ttg gaa tcg ctg ttc aat gct Glu Ser Arg Cys Phe Ala Ala Lys Leu Leu Glu Ser Leu Phe Asn Ala 90 95 100	2504	
tgt cgc gtc gta tcc gcg aga ggt act gcg gga gca aat tat acg cgc Cys Arg Val Val Ser Ala Arg Gly Thr Ala Gly Ala Asn Tyr Thr Arg 105 110 115	2552	
cgc tagtggccac aacttgggtt tactttcatg cgaccggac ctggtaacg Arg	2605	

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tttacgagcg ggcgtaaaat gtgtcgagtc tcgggtgata ttgtgggtcg gAACCTGCGC	4781
aaacggcgct tctaccggcg gaattttgtg ctaccagagg ggcacagcga gatcagtat	4841
atgggtgcct gtgagtaacgg agtgtatTTT gtgtcacaa cggggcgggc ggtgggtacc	4901
gttgacggcc ggttactcga ggacaccctg gagggttcg gtccgctcg gttggctca	4961
cggtgacacct gttccccgcc ataaggctca cgatgtcgtc accccctgtat atatTTTAA	5021
tttttatact gacaatgtta acgataatga ccgcgatcac aatcttaccgtcaagggtg	5081
ccaagcgtga atgtggggac gaccatttcg cgacccgttc cccattgaag gagcgcgtta	5141
ccgcccacgga gcaacagttt agcgacacgg agcagcgcatt tgacgaggc gAACGGTCGG	5201
gtgtggaaaa tttagcgcatacggcggaaa cattggagaa tatatcgggc gagctgggtgg	5261
agctgcaaaa ctcgacactcg tcaaagttt acgaaattgg caacgagctg gtgaacactgg	5321
atctgcgcgtt ccagtgccta gagtgagtgc cgaaatttcg taccagtgtt ttgacggtag	5381
ctgcaagtaa gagccaacga tgcccaaac ttactattt ctaatttcac tactactgtt	5441
cacaatgggtt gccgtgccta tcatgcgccta cccagccaa cctcccgagt gcaagtgcga	5501
ggagggctcg ggggtggacc tcaccaaact cacggctaga gtggacgagc tcgagcaaaa	5561
gcttggccccc atgaacacca ctttggccaa actgaacgcgac gacctgtcg agctgtccag	5621
ctccaggatgataaattt catacataaa cgtcgcacatc aatgagctgg ccgacagtat	5681
caaaacgatg gaccaacgcgt tgaagggtctt ggaggagag tgatataattt actgctgcac	5741
taaaaacgagg tgtataaattt ttatcatttt ttattatttt tcttggaaaag aaagaaatat	5801
aggcttaatc ggtggggaca ttgggggagt gggcgctcg acagggaaaca ttttcgcac	5861
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gatcatgaag cggacaagtgtt gtgcggatgtt tcgcgcgtcc atcggttat aggtgggttt	6161
gtggcccgtag taggtgcgtt gtacgcgcgtt cagttccgac cgagttgggtt gtgcgtgcact	6221
attacccaa cacttgtac ttttgtccatgtt acgttttttgc caccggctgtt ggcaatagac	6281
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aatttcacaa aaccgttcc gctgcgcac cccacgcgtcg atccatgccc ggtaaaccac	6401
ccgatgactg taacgattgc gcacactaag cccaaagataa ataccctccg tttcggcgctc	6461
cacagcgcgg tctaaacgcgtt ccagtcgttgc acctcattaa actcgcgcata	6521
caagtcgcgc acgaatttag ttagccgtt tcgattcatg ctgcgttagtt ccagccgagc	6581
cccgaaacca acctttatat accccgttat catgagagaa ttc	6624

<210> SEQ ID NO 34

<211> LENGTH: 118

<212> TYPE: PRT

<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 34

Met Asp Leu Tyr Val Arg Asp Ala Asp Cys Ala Val Val Phe Gly Arg	
1 5 10 15	

Asn Asn Ala Gln Ser Asn Trp Phe His Leu Asp Thr Leu Pro Ile Asn

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20	25	30	
Gly Glu Val Met Asn Val Ala Arg Lys Asn Asp Pro Leu Leu Trp Tyr			
35	40	45	
Ala Thr Val Gln Glu Asn Phe Tyr Thr Phe Arg Pro Leu Thr Ala Leu			
50	55	60	
Glu Leu Arg Glu Lys Gly Arg Phe Asp Gly Phe Tyr Pro Pro Thr Thr			
65	70	75	80
Asp His Trp Val Ile Glu Ser Arg Cys Phe Ala Ala Lys Leu Leu Glu			
85	90	95	
Ser Leu Phe Asn Ala Cys Arg Val Val Ser Ala Arg Gly Thr Ala Gly			
100	105	110	
Ala Asn Tyr Thr Arg Arg			
115			

<210> SEQ_ID NO 35
<211> LENGTH: 56
<212> TYPE: PRT
<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 35

Met Ser Leu Ser Trp Asp Ser Cys Gly Asn Arg Lys Gly Arg Asn Val			
1	5	10	15
Val Arg Phe Ser Gly Ala His Thr Gly Ala Arg Asn Asp Ser Val Asp			
20	25	30	
Phe Asn Phe Gly Cys Lys Ile Ser Ser Gln Thr Arg Pro Arg Val Ala			
35	40	45	
Gly Thr Gly Arg Thr Ser Ser Gly			
50	55		

<210> SEQ_ID NO 36
<211> LENGTH: 6624
<212> TYPE: DNA
<213> ORGANISM: mosquito baculovirus
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (2033)...(2218)

<400> SEQUENCE: 36

gaattctctc atgataacgg ggtatataaaa gggtggtttc ggggctcgcc tggAACCTAG	60
cagcatgaat cgaaagcggc taactaaatt cgtgcgcgac ttgtatcgcg agtttaatga	120
ggttcactgc gaacagagac tggaaagcggtt agaccgcgct gtggacgccc aaacggagg	180
tatttatctt gggcttagtg tgcgcaatcg ttacagtcat cgggtggttt accgggcatg	240
gatcgacggtt ggggtcgccc agcggaaactg gtttgtgaa attgaattac cacaagcggt	300
gctcgacgct aaccattaca ttttaattttt tttcggcaca cgagtctatt gccaacagcc	360
gtggctaaacg tacctggaca aaacgtacaa gtgttgggtt aatagtgcac gacaaccaac	420
tcgggtcgaa ctgaagcgcg tacctagcac ctactggcgc cacaacacca cctatataac	480
gatggacgccc cgatcatttc gaccacttgt ccgtttcatg atcgacgtcc acgtacgtac	540
ctgactgttt ctgccacccc ggaccctgtt accatgcact cttcagccac tgcggaggtt	600
tctgccagtc ctgttggacc cactacgaag acctagacga gttcgtgcgc tgtatgagg	660
gccagaccac ccacaaacccg aaccccatcg ccataacaat ggggctctgc gaataactgtc	720
cgagaaggca cccggtcggc gtgtccctgcc aaggctatcc agcgtgcgaa aaatgttccc	780
tgtcgcacgc cccactcccc caatgtcccc accgattaag cctatatttc tttctttca	840

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agaaaaataa	taaaaatga	taaaatttat	acacctcggtt	ttattgcagc	agtaaatata	900
tcactctccc	tccagcacct	tcaagcgttg	gtccatcggtt	ttgatactgt	cggccagctc	960
attgatggcg	acgtttatgt	atgaaaattt	atcatcactg	gagctggaca	gctccgacag	1020
gtcgtcggtt	agtttgcaca	agggtgggtt	catggggcca	agttttgtc	cgagctcgtc	1080
cactctagcc	gtgagtttgg	tgaggtccac	ccccgagccc	tcctcgact	tgcactcggtt	1140
aggttggct	gggttagcgc	tgatgagcac	ggccaccatt	gtgaccagta	ttagtagaaat	1200
tagaaatagt	aaagtttggg	gcatcggttgg	ctcttacttg	cagctaccgt	caaaccactg	1260
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tcaatcgct	gctccgtgtc	gtctcaactgt	tgctccgtgg	cggttaacgc	cgcccttcaat	1500
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gaccgaaacc	ctccagggtt	tcctcgagta	accggccgtc	aacggtcacc	accgccccggc	1740
ccgttcgtga	caccaaatac	actccgtact	cacaggcacc	catataactg	atctcgctgt	1800
gcccctctgg	tagcaca	ttccgcccgtt	agaagcgccg	tttgcgcagg	ttccgcacca	1860
caatatcaac	cggactcga	cacatttac	gcccgtcg	aaactcg	tgcagcgca	1920
gcttgctgct	tggtaagca	caccgaat	ggcgattat	acggccccgg	gcggtaat	1980
tat	tgcgttgc	taccagtccc	gcacacacaa	gcgtccggag	tgaacgcttg	2038
				ct cga gca		
				Arg Ala		
				1		
agt tta tct cca att gac	cgc cg	g tac aca cat acg	gtt gca gtt tgt			2086
Ser Leu Ser Pro Ile Asp Arg	Arg Tyr Thr His	Thr Val Ala Val Cys				
5	10	15				
tat cgt cgg tga aaa	tgt cgc gat	agg ttg aaa ggc	agg att gat tta			2134
Tyr Arg Arg	* Lys Cys Arg	Asp Arg Leu Lys	Gly Arg Ile Asp Leu			
20	25	30				
taa cga att cgt ctg cag tga	ata ccc gta	aaa ttc cat gct	ctt cga			2182
* Arg Ile Arg Leu Gln	* Ile Pro Val Lys	Phe His Ala Leu Arg				
35	40	45				
cac aat ttc gct tct cgg	gaa tag att tat	gat ccg tgctgcagaa				2228
His Asn Phe Ala Ser Arg Glu	* Ile Tyr Asp Pro					
50	55					
ccgcctatg cacgatgaaa	ctcctccgtc	tctggtcaaa	gcgcagttac	gttgcagtc		2288
ccgattatca atacacggtt	atttgggtt	gtggcaatct	acgtgcttag	agccggcgaa		2348
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ggcgttgg	gctagaaatt	ttgcacccga	agttaaaatc	aactgaatca	ttacgagcac	2468
cagtatgagc	accactaaac	cgtacaacat	ttcttccctt	tctat	ttcca caggaatccc	2528
aacttaaaga	catttggaaac	actttcgaga	agcccggagga	gcgc	aaatgg	2588
taagcgacaa	ggtgtgggtt	ccaccggaaag	aattcgacac	aatgagtgaa	ttcatcgaga	2648
ccgtacacta	caacaccgac	ccgatccgg	cgagctatgg	catttgggg	ctgcacaccc	2708
gcgggaaccg	gggctgccga	gagtgggtga	ttgatatcga	tttggaaact	gacgaccccg	2768
agttggccaa	catttgc	tttgcaccc	aatgttcttc	ttcggtaccg		2828
aaaacattaa	agtttaccac	acggcaacg	acggcatcca	catttggctc	aacccggccca	2888

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acttcccggt ggactcgagc gccgaattgc gcggattcta cctcgccgcc atgcagctac	2948
ccaaaggtaa ggaggaaacta cacagactgg tgccgaccac cgagtgcagg ttgtttgcg	3008
acgcccactg ctgcggaatc gattcaagc ccaagatgcg catcatcgac accccaccca	3068
atccccacgga accgatttcg tttccgaggt gctttgtgcg cgctctctgc tgcaacgaaa	3128
cctatatgaa cgaatgaca tcgattatac gcaacaaccg ggacgtggtg agcacccgtca	3188
ccgacgtgtg gagactcttt tggccgcca tagatgcggg cctgtttcaa tcgcccagcta	3248
gactctgccg tgcacccctc agttaccact tgaagggcgg tcggcttcg cgtcgtattg	3308
acttggatga atatTTAA aatgattgaa ataaaaaggTT ttattaacaa tgactcattg	3368
aagtTTTtat tcccccaac atcacaagtt caaccccgac tgccgctcca ttaaatgaaa	3428
aatgttcatt tggtagcagc actttaacgg gtccactttt gtggggccgc caaatgttgg	3488
gctccatatg gaaaagttag cccaaccaag acgggtccac ttttgtggg cccacatttgc	3548
cgggtgtaaa ggggtgggt ttgggttggaa ataaaataaa aatTTTctaa ctctaaccagg	3608
tattattata tttgatcaca ttttcatca caacatttcg ggggtgtgggt gctttatca	3668
cagatagacc accggcgaat cgtacacact gggcgcttt taggtcgacg ttcacacagt	3728
gacccaagtt gcaaggctgt ccagttcggt gcagtaccac catacgagcc tcccaataat	3788
gttccagcag aatTTTgcgaa agatcgcgTT gatTTTaaat atcgagcaat agcaccaccg	3848
gaccgttgac cgtaacatgg tttagtgcac gaattgcagt gccaaggatct ccagtagtgc	3908
ggtaccaaca ttggtaacg ttattcacca ataccatcca agtttcgtgc aggctcgccc	3968
cgtcaactat ggtgtaaaaa agttcaaat ctaccagcaa atttgcac tggttaacca	4028
ggtccgggtc gcatgaaagt aacaccaagt tggggact agcggcgcgt ataatttgc	4088
cccgcagtac ctctcgccga tacgacgcga caagcattga acagcgattc caacaacttg	4148
gctgcgaagc acctcgactc gataaccccg tggccgttag ttgggtggata gaatccgtca	4208
aagcaccctt ttctctcag ttccagcgcc gtgagcggtc gaaaggataaaaatttctcc	4268
tgaactgtgg cgtaccataa gagaggatcg ttttacgag cgacattcat aaccccccgg	4328
tttataaggca aagtgcgag gtgaaaccag tttagattgag cgttattacg gccaacacgc	4388
accgcgcagt ccgcacatcgc aacatcacaaa tccatcccta tcaccgcaga ccgggtggagt	4448
cattgaacca tggcccttggt gcacattgaa cagcgcggat tgtcgtgcta tgtcgtgggt	4508
ttcgaggccca acgttggacc cgcacctgtac cagtgatttg tcgattgcaaa accccaccc	4568
atgcgtata tagacttaa ccattccggaa ttttgcac agctgaggcc aatcgatggg	4628
cacaacccccc acagttccac cagtggggat tacatcgatc tatggcttgc gctactgaac	4688
gaggctgcta tgaagtccggg ctggatgaa gagggtggat tagggagctg ttgagcaaac	4748
atTTTcgctt ggaagaaagg gaagagaaat aaacaaacaa ctttagtttgc catcatcaag	4808
tgttttattt ttctaaaact gcccctcgatt tctccaccaaa accctccata aattgcagct	4868
catcgggaa gcatggccg accagggtcca gcatggctt cggcgttgcgatcgcacat	4928
cgtatTTTaa acagtagccaa aagttagtact ccaaatctcg actctcgatc atcacttctg	4988
taccgtcgca caccactcgatc atggagatgg accgcaggcgc catgtcgtaa tgtaaaaacta	5048
gaagaaactt ttccgggtgcc aatgaggtaa cttctccgtat ctcgagcaggc tcttggggca	5108
gctcgaagggtt gatcatTTTC ggttaaccgtt gcccgtgtat gaggaccgtat tttcgtggcc	5168
actcccaactc ggcggggcgcatttggccca aatcgatggcc cgtcgccgtt acgttgc	5228

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agctgctatt tatgtttag gcttcgtact gtacgaagcc ccgcaccgcc aactgggtgt	5288
ccacgtataa aaatctcgtc aacgggtggc gcaggatccg aaagatgggt cgacgatttt	5348
cagctccaac gtgcacaaat gtacccgaaa agctgtacat gtttgcgggt aagttcagct	5408
actctttaaa atatcgact ataaatcgat tcacgctcac caatcgtagc agtattcaca	5468
caatgttcta ctctgttagaa gttcgcgtat ttagtacgga gattccgtcg cagtcgctgc	5528
accactccca ccatacgcc ataccgttcg ataaagatag atggaccgtc gatggcattt	5588
taccgaacga tataccgctc gaccacacga tacgggttg tggttaccgtc aggggttagta	5648
aaaaattttc ctgcgtatgg cgagagacca cctacaagtgc ggaaatgtg tacgatccac	5708
cactagagta ccagttggag aagctgcccgg gctgtcagta tagcgatcta gcgttaagga	5768
taatcgagaa gttttagcgc gctatgaagt acacgataga agtcgatttc actgcaaata	5828
aatctcaaag tttggattta taaaccaccc gtctttcatt gttAACCGC ccccaacccca	5888
acgatgttac aagttccct agtaggaccc cacttcacac tcgtgcgtcg cagtggcgat	5948
ttgcgggtgcc agtttctatt accaccgtgg gccgcactgg acaacagttt gatgctcg	6008
gtgcagttggg atcagcgcaa ctataccctc aactggccgg gcgaaatatt ttacgggtgg	6068
attgcagcac gaccgggtgac accgcacatg ctcaagtggcgt gctaccacct cgcggccac	6128
cctgagccca actttaccgt ggaagaaaaa caacctggcgt gtgatattacg acaccctta	6188
taataaaaaa aaaatcgctt caaacaggga caataaaacc cacaagtgtt tagagttttt	6248
tttttatttt attttccaa gtatattggaa actggaaaga aataataaca acaataataaa	6308
caataataat atcaataaaa aaggattttcg atttatgact gtgcgcgcgc gcacaacagg	6368
gccggcttct tggttacaaa ctcaacttcc tgattctcg ccgtagcgcc cgggagctca	6428
tgcttgcgtca ctggtaacct gcacgggata gaggaacgtt tccaccctat cgagcaacac	6488
cccactttca ccgaccaact cactcaacca tggccgattt ggacacacag ctggggact	6548
ttgtcgaccc gggcaacat ttctcgcc tccaggtcgt gcggtatcgta agaatctcg	6608
acacggcgcc aagctt	6624

<210> SEQ ID NO 37

<211> LENGTH: 58

<212> TYPE: PRT

<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 37

Arg Ala Ser Leu Ser Pro Ile Asp Arg Arg Tyr Thr His Thr Val Ala			
1	5	10	15

Val Cys Tyr Arg Arg Lys Cys Arg Asp Arg Leu Lys Gly Arg Ile Asp			
20	25	30	

Leu Arg Ile Arg Leu Gln Ile Pro Val Lys Phe His Ala Leu Arg His			
35	40	45	

Asn Phe Ala Ser Arg Glu Ile Tyr Asp Pro		
50	55	

<210> SEQ ID NO 38

<211> LENGTH: 1300

<212> TYPE: DNA

<213> ORGANISM: mosquito baculovirus

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (539)...(916)

<400> SEQUENCE: 38

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actgcagctc cacgtgacg aagttaacct gctcgaaat cgaaccaccg cggttgggt	60
taattttagt cgtggtagc gcaaaaatcga agaatttctt cagctcactg tagagaacg	120
cggccagctt catctttcg ttcaaattga tctccgtact accaccgaca attttggta	180
gctccaccac gtactcctcc aagtccaggt tggtagcag gtcgagctt actcgcgccc	240
ggcccaactg catcatcaca ctgcgaagcg cctcacggc cagcgtcacc tcgcccgtt	300
tagactcctt tggccctcg accgctttct ggatttgtt ctcgacgtca aaacatctag	360
acttgaactc gctgtccgag atggggctgc cgagcacatc gatcatggtg ctcaagtcgt	420
tcatatagcc cacaatttca cccaccagcg gaccggcag ttggccgac tttgtctcgc	480
aatatttct caaattatcc aagcaaattt tcagctgacg gcggggccata ttgttagta	538
atg cac cac ctc gcg ggc cct ctc ggt gca gat ttt aat gtg cat att Met His His Leu Ala Gly Pro Leu Gly Ala Asp Phe Asn Val His Ile	586
1 5 10 15	
ttg caa ttt gaa aat ttt ctc agc caa ctc cat cga agg ggt ttc gcg Leu Gln Phe Glu Asn Phe Leu Ser Gln Leu His Arg Arg Gly Phe Ala	634
20 25 30	
gta cga cat cag cat gct gtc cag cat gaa ctt gtt ttg ctg ctc cag Val Arg His Gln His Ala Val Gln His Glu Leu Val Leu Leu Gln	682
35 40 45	
ctg aca atc gtc gcc cgt ggc aac att ttt atc gaa gct caa gtc ctt Leu Thr Ile Val Ala Arg Gly Asn Ile Phe Ile Glu Ala Gln Val Leu	730
50 55 60	
ggt gca ctc gtt caa ctt gga ccg caa agc ctc aat ttc acg cgt ggc Gly Ala Leu Val Gln Leu Gly Pro Gln Ser Leu Asn Phe Thr Arg Gly	778
65 70 75 80	
cac cgc caa atc ctc gcc aac gtt ttg cgc atc cga ata tac acc ctc His Arg Gln Ile Leu Ala Asn Val Leu Arg Ile Arg Ile Tyr Thr Leu	826
85 90 95	
gag att ggc aat ttt act ctt gag ctg cac aat gtt cgc ctc gag gtc Glu Ile Gly Asn Phe Thr Leu Glu Leu His Asn Val Arg Leu Glu Val	874
100 105 110	
gga aat ttt ctc cat ata ccg ctt caa gtt gcc gct gtc ggt Gly Asn Phe Leu His Ile Pro Leu Gln Val Ala Ala Val Gly	916
115 120 125	
taacagcttc gaaatgcctt ccctcacatc accccgaaaa ccgttctctt ccagctcaac	976
ttttatttcc ctctccagg ttagccgct atcgtacagc ttctccgacc gcttcaaacc	1036
gctgtactcg gcgctcaact gtagcaaact ttgttccaaa ccgtcgacgg ttagcaaacc	1096
cttttccctt agaatatttt caacacgttc gatcaggctcg aggttggtca tcgcgtatgtc	1156
gtactccaca gcctgcttgt tcttggccctc tcgacccaga attatttctt cctgaaggtc	1216
tgttataaaa tcgtccacct cctggccga catcgtgtcc ataaacaacg cagcatcggtt	1276
cgcgatttta cgcagccccct gcag	1300

<210> SEQ ID NO 39

<211> LENGTH: 126

<212> TYPE: PRT

<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 39

Met His His Leu Ala Gly Pro Leu Gly Ala Asp Phe Asn Val His Ile
1 5 10 15Leu Gln Phe Glu Asn Phe Leu Ser Gln Leu His Arg Arg Gly Phe Ala
20 25 30

Val Arg His Gln His Ala Val Gln His Glu Leu Val Leu Leu Gln

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35	40	45
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Leu Thr Ile Val Ala Arg Gly Asn Ile Phe Ile Glu Ala Gln Val Leu
 50 55 60

Gly Ala Leu Val Gln Leu Gly Pro Gln Ser Leu Asn Phe Thr Arg Gly
 65 70 75 80

His Arg Gln Ile Leu Ala Asn Val Leu Arg Ile Arg Ile Tyr Thr Leu
 85 90 95

Glu Ile Gly Asn Phe Thr Leu Glu Leu His Asn Val Arg Leu Glu Val
 100 105 110

Gly Asn Phe Leu His Ile Pro Leu Gln Val Ala Ala Val Gly
 115 120 125

<210> SEQ ID NO 40
<211> LENGTH: 1300
<212> TYPE: DNA
<213> ORGANISM: mosquito baculovirus
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (858)...(1208)

<400> SEQUENCE: 40

actgcagctc cacgtgacg aagttaacct gctcgaaat cgaaccaccg cggttgggt taattttag cgtgtgacg gcaaatcga agaatttctt cagctactg tagtagaacg cggccagctt cattttcg ttcaaattga tctccgtact accaccgaca attttgtca gctccaccac gtactcctcc aagtccaggt tgggtacag gtcgagctt actcgcccc ggcccaactg catcatcaca ctgcgaagcg cctcacgggc cagcgtcacc tcgcccgtt tagactcctt tgtggctcg accgcttctt ggattttgtta ctcgacgtca aaacatctag acttgaactc gctgtccgag atggggctgc cgagcacatc gatcatggtg ctcaagtctg tcatatagcc cacaatttca cccaccagcg gaccggcag ttccggccac tttgtctcgc gaatatttctt caaattatcc aagcaaattt tcagctgacg gccccata ttgttagaat gcaccacactc gcccccttc tcggcaga tttaatgtg catattttgc aatttggaaa ttttctcgc caactccatc gaagggttcc cgcgggtacga catcagcatg ctgtccagca tgaacttgc ttgctgctcc agctgacaat cgtcgccgtt gccaacattt ttatcgaagc tcaagtccctt ggtgactcg ttcaacttgg accgcacccg ctcattttca cgcgtggcca ccgcacccatc ctcgcacccg ttttgcgcattt ccgaatatac accctcgaga ttggcaattt tactcttgcgat ctgcaca atg ttc gcc tcg agg tcg gaa att ttc tcc ata Met Phe Ala Ser Arg Ser Glu Ile Phe Ser Ile 1 5 10	60 120 180 240 300 360 420 480 540 600 660 720 780 840 890 938 986 1034 1082 1130
--	--

tac cgc ttc aag ttg ccg ctg tcg gtt aac agc ttc gaa atg ccc tcc
 Tyr Arg Phe Lys Leu Pro Leu Ser Val Asn Ser Phe Glu Met Pro Ser
 15 20 25

ctc aca tca ccc cga aaa ccg ttc tcc tcc agc tca act ttt att tcc
 Leu Thr Ser Pro Arg Lys Pro Phe Ser Ser Ser Thr Phe Ile Ser
 30 35 40

ctc tcc agg ttt acg gcg cta tcg tac agc ttc tcc gac cgc ttc aaa
 Leu Ser Arg Phe Thr Ala Leu Ser Tyr Ser Phe Ser Asp Arg Phe Lys
 45 50 55

cgg ctg tac tcg gcg ctc aac tgt agc aaa ctt tgt tcc aaa ccg tcg
 Arg Leu Tyr Ser Ala Leu Asn Cys Ser Lys Leu Cys Ser Lys Pro Ser
 60 65 70 75

acg gtt agc aaa ccc ttt tcc ttt aga ata ttt tca aca cgt tcg atc
 Thr Val Ser Lys Pro Phe Ser Phe Arg Ile Phe Ser Thr Arg Ser Ile
 80 85 90

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agg tcg agg ttg gtc atc gcg atg tcg tac tcc aca gcc tgc ttg ttc
 Arg Ser Arg Leu Val Ile Ala Met Ser Tyr Ser Thr Ala Cys Leu Phe
 95 100 105 1178

ttg gcc tct cga ccc aga att att ttc tcc tgaaggctcg ttataaaatc
 Leu Ala Ser Arg Pro Arg Ile Ile Phe Ser
 110 115 1228

gtccacacctcc tggccgaca tcgtgtccat aaacaacgca gcatcggtcg cgattttacg 1288
 cagccccctgc ag 1300

<210> SEQ ID NO 41
<211> LENGTH: 117
<212> TYPE: PRT
<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 41

Met Phe Ala Ser Arg Ser Glu Ile Phe Ser Ile Tyr Arg Phe Lys Leu
 1 5 10 15

Pro Leu Ser Val Asn Ser Phe Glu Met Pro Ser Leu Thr Ser Pro Arg
 20 25 30

Lys Pro Phe Ser Ser Ser Ser Thr Phe Ile Ser Leu Ser Arg Phe Thr
 35 40 45

Ala Leu Ser Tyr Ser Phe Ser Asp Arg Phe Lys Arg Leu Tyr Ser Ala
 50 55 60

Leu Asn Cys Ser Lys Leu Cys Ser Lys Pro Ser Thr Val Ser Lys Pro
 65 70 75 80

Phe Ser Phe Arg Ile Phe Ser Thr Arg Ser Ile Arg Ser Arg Leu Val
 85 90 95

Ile Ala Met Ser Tyr Ser Thr Ala Cys Leu Phe Leu Ala Ser Arg Pro
 100 105 110

Arg Ile Ile Phe Ser
 115

<210> SEQ ID NO 42
<211> LENGTH: 1300
<212> TYPE: DNA
<213> ORGANISM: mosquito baculovirus
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)...(1299)

<400> SEQUENCE: 42

ctg cag ggg ctg cgt aaa atc gcg aac gat gct gcg ttg ttt atg gac 48
 Leu Gln Gly Leu Arg Lys Ile Ala Asn Asp Ala Ala Leu Phe Met Asp
 1 5 10 15

acg atg tcg gac cag gag gtg gac gat ttt ata aca gac ctt cag gag 96
 Thr Met Ser Asp Gln Glu Val Asp Asp Phe Ile Thr Asp Leu Gln Glu
 20 25 30

aaa ata att ctg ggt cga gag gcc aag aac aag cag gct gtg gag tac 144
 Lys Ile Ile Leu Gly Arg Glu Ala Lys Asn Lys Gln Ala Val Glu Tyr
 35 40 45

gac atc gcg atg acc aac ctc gac ctg atc gaa cgt gtt gaa aat att 192
 Asp Ile Ala Met Thr Asn Leu Asp Leu Ile Glu Arg Val Glu Asn Ile
 50 55 60

cta aag gaa aag ggt ttg cta acc gtc gac ggt ttg gaa caa agt ttg 240
 Leu Lys Glu Lys Gly Leu Leu Thr Val Asp Gly Leu Glu Gln Ser Leu
 65 70 75 80

cta cag ttg agc gcc gag tac agc cgt ttg aag cgg tcg gag aag ctg 288
 Leu Gln Leu Ser Ala Glu Tyr Ser Arg Leu Lys Arg Ser Glu Lys Leu
 85 90 95

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tac gat agc gcc gta aac ctg gag agg gaa ata aaa gtt gag ctg gag Tyr Asp Ser Ala Val Asn Leu Glu Arg Glu Ile Lys Val Glu Leu Glu 100 105 110	336
gag aac ggt ttt cgg ggt gat gtg agg gag ggc att tcg aag ctg tta Glu Asn Gly Phe Arg Gly Asp Val Arg Glu Gly Ile Ser Lys Leu Leu 115 120 125	384
acc gac agc ggc aac ttg aag cgg tat atg gag aaa att tcc gac ctc Thr Asp Ser Gly Asn Leu Lys Arg Tyr Met Glu Lys Ile Ser Asp Leu 130 135 140	432
gag gcg aac att gtg cag ctc aag agt aaa att gcc aat ctc gag ggt Glu Ala Asn Ile Val Gln Leu Lys Ser Lys Ile Ala Asn Leu Glu Gly 145 150 155 160	480
gta tat tcg gat gcg caa aac gtt ggc gag gat ttg gcg gtg gcc acg Val Tyr Ser Asp Ala Gln Asn Val Gly Glu Asp Leu Ala Val Ala Thr 165 170 175	528
cgt gaa att gag gct ttg cgg tcc aag ttg aac gag tgc acc aag gac Arg Glu Ile Glu Ala Leu Arg Ser Lys Leu Asn Glu Cys Thr Lys Asp 180 185 190	576
ttg agc ttc gat aaa aat gtt gcc acg ggc gac gat tgt cag ctg gag Leu Ser Phe Asp Lys Asn Val Ala Thr Gly Asp Asp Cys Gln Leu Glu 195 200 205	624
cag caa aac aag ttc atg ctg gac agc atg ctg atg tcg tac cgc gaa Gln Gln Asn Lys Phe Met Leu Asp Ser Met Leu Met Ser Tyr Arg Glu 210 215 220	672
acc cct tcg atg gag ttg gct gag aaa att ttc aaa ttg caa aat atg Thr Pro Ser Met Glu Leu Ala Glu Lys Ile Phe Lys Leu Gln Asn Met 225 230 235 240	720
cac att aaa atc tgc acc gag agg gcc cgc gag gtg gtg cat tac tac His Ile Lys Ile Cys Thr Glu Arg Ala Arg Glu Val Val His Tyr Tyr 245 250 255	768
aat atg gcc cgc cgt cag ctg aaa att tgc ttg gat aat ttg aga aat Asn Met Ala Arg Arg Gln Leu Lys Ile Cys Leu Asp Asn Leu Arg Asn 260 265 270	816
att cgc gag aca aag tcg gcc gaa ctg ccc ggt ccg ctg gtg ggt gaa Ile Arg Glu Thr Lys Ser Ala Glu Leu Pro Gly Pro Leu Val Gly Glu 275 280 285	864
att gtg ggc tat atg aac gac acc ttg agc acc atg atc gat gtg ctc ggc Ile Val Gly Tyr Met Asn Asp Leu Ser Thr Met Ile Asp Val Leu Gly 290 295 300	912
agc ccc atc tcg gac agc gag ttc aag tct aga tgt ttt gac gtc gag Ser Pro Ile Ser Asp Ser Glu Phe Lys Ser Arg Cys Phe Asp Val Glu 305 310 315 320	960
tac aaa atc cag aaa gcg gtc gag gcc aca aag gag tct aaa cag ggc Tyr Lys Ile Gln Lys Ala Val Glu Ala Thr Lys Glu Ser Lys Gln Gly 325 330 335	1008
gag gtg acg ctg gcc cgt gag gcg ctt cgc agt gtg atg atg cag ttg Glu Val Thr Leu Ala Arg Glu Ala Leu Arg Ser Val Met Met Gln Leu 340 345 350	1056
ggc cgg gcg cga gta aag ctc gac ctg tac aac aac ctg gac ttg gag Gly Arg Ala Arg Val Lys Leu Asp Leu Tyr Asn Asn Leu Asp Leu Glu 355 360 365	1104
gag tac gtg gtg gag ctg aac aaa att gtc ggt ggt agt acg gag atc Glu Tyr Val Val Glu Leu Asn Lys Ile Val Gly Gly Ser Thr Glu Ile 370 375 380	1152
aat ttg aac gaa aag atg aag ctg gcc gcg ttc tac tac agt gag ctg Asn Leu Asn Glu Lys Met Lys Leu Ala Ala Phe Tyr Tyr Ser Glu Leu 385 390 395 400	1200
aag aaa ttc ttc gat ttt gcc gtc acc acg ctc aaa att aac ccc aac Lys Lys Phe Phe Asp Phe Ala Val Thr Thr Leu Lys Ile Asn Pro Asn	1248

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405

410

415

cgc ggt ggt tcg att tcc gag cag gtt aac ttc gtc agc gtg gag ctg
 Arg Gly Gly Ser Ile Ser Glu Gln Val Asn Phe Val Ser Val Glu Leu
 420 425 430

cag t
 Gln

<210> SEQ_ID NO 43
 <211> LENGTH: 433
 <212> TYPE: PRT
 <213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 43

Leu Gln Gly Leu Arg Lys Ile Ala Asn Asp Ala Ala Leu Phe Met Asp
 1 5 10 15

Thr Met Ser Asp Gln Glu Val Asp Asp Phe Ile Thr Asp Leu Gln Glu
 20 25 30

Lys Ile Ile Leu Gly Arg Glu Ala Lys Asn Lys Gln Ala Val Glu Tyr
 35 40 45

Asp Ile Ala Met Thr Asn Leu Asp Leu Ile Glu Arg Val Glu Asn Ile
 50 55 60

Leu Lys Glu Lys Gly Leu Leu Thr Val Asp Gly Leu Glu Gln Ser Leu
 65 70 75 80

Leu Gln Leu Ser Ala Glu Tyr Ser Arg Leu Lys Arg Ser Glu Lys Leu
 85 90 95

Tyr Asp Ser Ala Val Asn Leu Glu Arg Glu Ile Lys Val Glu Leu Glu
 100 105 110

Glu Asn Gly Phe Arg Gly Asp Val Arg Glu Gly Ile Ser Lys Leu Leu
 115 120 125

Thr Asp Ser Gly Asn Leu Lys Arg Tyr Met Glu Lys Ile Ser Asp Leu
 130 135 140

Glu Ala Asn Ile Val Gln Leu Lys Ser Lys Ile Ala Asn Leu Glu Gly
 145 150 155 160

Val Tyr Ser Asp Ala Gln Asn Val Gly Glu Asp Leu Ala Val Ala Thr
 165 170 175

Arg Glu Ile Glu Ala Leu Arg Ser Lys Leu Asn Glu Cys Thr Lys Asp
 180 185 190

Leu Ser Phe Asp Lys Asn Val Ala Thr Gly Asp Asp Cys Gln Leu Glu
 195 200 205

Gln Gln Asn Lys Phe Met Leu Asp Ser Met Leu Met Ser Tyr Arg Glu
 210 215 220

Thr Pro Ser Met Glu Leu Ala Glu Lys Ile Phe Lys Leu Gln Asn Met
 225 230 235 240

His Ile Lys Ile Cys Thr Glu Arg Ala Arg Glu Val Val His Tyr Tyr
 245 250 255

Asn Met Ala Arg Arg Gln Leu Lys Ile Cys Leu Asp Asn Leu Arg Asn
 260 265 270

Ile Arg Glu Thr Lys Ser Ala Glu Leu Pro Gly Pro Leu Val Gly Glu
 275 280 285

Ile Val Gly Tyr Met Asn Asp Leu Ser Thr Met Ile Asp Val Leu Gly
 290 295 300

Ser Pro Ile Ser Asp Ser Glu Phe Lys Ser Arg Cys Phe Asp Val Glu
 305 310 315 320

Tyr Lys Ile Gln Lys Ala Val Glu Ala Thr Lys Glu Ser Lys Gln Gly
 325 330 335

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Glu Val Thr Leu Ala Arg Glu Ala Leu Arg Ser Val Met Met Gln Leu
340 345 350

Gly Arg Ala Arg Val Lys Leu Asp Leu Tyr Asn Asn Leu Asp Leu Glu
355 360 365

Glu Tyr Val Val Glu Leu Asn Lys Ile Val Gly Gly Ser Thr Glu Ile
370 375 380

Asn Leu Asn Glu Lys Met Lys Leu Ala Ala Phe Tyr Tyr Ser Glu Leu
385 390 395 400

Lys Lys Phe Phe Asp Phe Ala Val Thr Thr Leu Lys Ile Asn Pro Asn
405 410 415

Arg Gly Gly Ser Ile Ser Glu Gln Val Asn Phe Val Ser Val Glu Leu
420 425 430

Gln

<210> SEQ ID NO 44

<211> LENGTH: 1017

<212> TYPE: DNA

<213> ORGANISM: mosquito baculovirus

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (85)...(966)

<400> SEQUENCE: 44

ctgcagcgca tattcggacct cccaaatacggt gagggtggccca cgggtgtcccg aaatggggac 60

caacttttacg agccccactt ggtg atg cgg ccc gac gaa ccg act atg cct 111
Met Arg Pro Asp Glu Pro Thr Met Pro
1 5

atg cgt gaa ttt gac acc ggt tta cga cgt gga gac caa cag gtg ctc 159
Met Arg Glu Phe Asp Thr Gly Leu Arg Arg Gly Asp Gln Gln Val Leu
10 15 20 25

aac agg ttg cgc atg acc tcg tcc gag cgg gct ggg ctc aac aat ata 207
Asn Arg Leu Arg Met Thr Ser Ser Glu Arg Ala Gly Leu Asn Asn Ile
30 35 40

cgg ggc aat tcg ctg ccc gat aat ctg tac cag cgg gtg cgc gca gac 255
Arg Gly Asn Ser Leu Pro Asp Asn Leu Tyr Gln Ala Val Arg Ala Asp
45 50 55

gag gcc gca att cgc gtt agg gat ccg aac ttg gcc aac gcg aga acc 303
Glu Ala Ala Ile Arg Val Arg Asp Pro Asn Leu Ala Asn Ala Arg Thr
60 65 70

gag cag gaa att acg gat gca ctt gcg cgt cat ccg agg cta cgt gac 351
Glu Gln Glu Ile Thr Asp Ala Leu Ala Arg His Pro Arg Leu Arg Asp
75 80 85

cgg ctt acg gcc ggt ggc gtg atc aag ggt gca ggt gtt tca ctt gta 399
Arg Leu Thr Ala Gly Gly Val Ile Lys Gly Ala Gly Val Ser Leu Val
90 95 100 105

att gta ggt ggg gct ctg ctc gcg gcc gag ctc tac caa tat ttg aat 447
Ile Val Gly Gly Ala Leu Leu Ala Ala Glu Leu Tyr Gln Tyr Leu Asn
110 115 120

cgt atg ggt ggt gcg ttt att gaa caa cgt gag gcg gac ggt tcg gtg 495
Arg Met Gly Gly Ala Phe Ile Glu Gln Arg Glu Ala Asp Gly Ser Val
125 130 135

gtg cgc cat tat tta ctt tgg aga tcc tgc ggt atg gat ccg tct gtg 543
Val Arg His Tyr Leu Leu Trp Arg Ser Cys Gly Met Asp Pro Ser Val
140 145 150

gtt tcg ttg gag gag gtt ttc ccg ggc gaa tcg ggt gac ccc att tac 591
Val Ser Leu Glu Glu Val Phe Pro Gly Glu Ser Gly Asp Pro Ile Tyr
155 160 165

gat agc gtt ggg gag gcc caa gcc att tgc agc ggt tat aat aaa agt 639

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Asp Ser Val Gly Glu Ala Gln Ala Ile Cys Ser Gly Tyr Asn Lys Ser
 170 175 180 185
 gta gaa cga agt gtt tgc cgc caa gcg gac gtg ttg gcc gag ccg tcc 687
 Val Glu Arg Ser Val Cys Arg Gln Ala Asp Val Leu Ala Glu Pro Ser
 190 195 200
 agc caa caa ttt tta gac gca cgt aca ctg cca gaa aac gct cac att 735
 Ser Gln Gln Phe Leu Asp Ala Arg Thr Leu Pro Glu Asn Ala His Ile
 205 210 215
 tac tgc gtt gag ccg ggt acg ttg gga cga ctg gtg gcc gac ctc ggg 783
 Tyr Cys Val Glu Pro Gly Thr Leu Gly Arg Leu Val Ala Asp Leu Gly
 220 225 230
 cta gca gat tta gtt gac gct gta ggc ggt tcg gtc agt ggg agc agc 831
 Leu Ala Asp Leu Val Asp Ala Val Gly Gly Ser Val Ser Gly Ser Ser
 235 240 245
 ggt aac agc agc ggc aag agc tcc ggc aac ccg ctg att ctg att agt 879
 Gly Asn Ser Ser Gly Lys Ser Ser Gly Asn Pro Leu Ile Leu Ile Ser
 250 255 260 265
 gcg ttc gtc gtg tta att ata ata atc ttc gtt gta gtc ttc ggt tat 927
 Ala Phe Val Val Leu Ile Ile Ile Ile Phe Val Val Val Phe Gly Tyr
 270 275 280
 tcc cgc acc cgt cgg aac tca gac gcg gat cgc acg ata taagtagaat 976
 Ser Arg Thr Arg Arg Asn Ser Asp Ala Asp Arg Thr Ile
 285 290
 tgtgcttcta taagcaactg aaagtgaagc taaaacctgca g 1017

<210> SEQ ID NO 45
 <211> LENGTH: 294
 <212> TYPE: PRT
 <213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 45

Met Arg Pro Asp Glu Pro Thr Met Pro Met Arg Glu Phe Asp Thr Gly
 1 5 10 15
 Leu Arg Arg Gly Asp Gln Gln Val Leu Asn Arg Leu Arg Met Thr Ser
 20 25 30
 Ser Glu Arg Ala Gly Leu Asn Asn Ile Arg Gly Asn Ser Leu Pro Asp
 35 40 45
 Asn Leu Tyr Gln Ala Val Arg Ala Asp Glu Ala Ala Ile Arg Val Arg
 50 55 60
 Asp Pro Asn Leu Ala Asn Ala Arg Thr Glu Gln Glu Ile Thr Asp Ala
 65 70 75 80
 Leu Ala Arg His Pro Arg Leu Arg Asp Arg Leu Thr Ala Gly Gly Val
 85 90 95
 Ile Lys Gly Ala Gly Val Ser Leu Val Ile Val Gly Gly Ala Leu Leu
 100 105 110
 Ala Ala Glu Leu Tyr Gln Tyr Leu Asn Arg Met Gly Gly Ala Phe Ile
 115 120 125
 Glu Gln Arg Glu Ala Asp Gly Ser Val Val Arg His Tyr Leu Leu Trp
 130 135 140
 Arg Ser Cys Gly Met Asp Pro Ser Val Val Ser Leu Glu Glu Val Phe
 145 150 155 160
 Pro Gly Glu Ser Gly Asp Pro Ile Tyr Asp Ser Val Gly Glu Ala Gln
 165 170 175
 Ala Ile Cys Ser Gly Tyr Asn Lys Ser Val Glu Arg Ser Val Cys Arg
 180 185 190
 Gln Ala Asp Val Leu Ala Glu Pro Ser Ser Gln Gln Phe Leu Asp Ala
 195 200 205

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Arg Thr Leu Pro Glu Asn Ala His Ile Tyr Cys Val Glu Pro Gly Thr
210          215          220

Leu Gly Arg Leu Val Ala Asp Leu Gly Leu Ala Asp Leu Val Asp Ala
225          230          235          240

Val Gly Gly Ser Val Ser Gly Ser Ser Gly Asn Ser Ser Gly Lys Ser
245          250          255

Ser Gly Asn Pro Leu Ile Leu Ile Ser Ala Phe Val Val Leu Ile Ile
260          265          270

Ile Ile Phe Val Val Phe Gly Tyr Ser Arg Thr Arg Arg Asn Ser
275          280          285

Asp Ala Asp Arg Thr Ile
290

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<210> SEQ ID NO 46
<211> LENGTH: 1017
<212> TYPE: DNA
<213> ORGANISM: mosquito baculovirus
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (682)...(882)

<400> SEQUENCE: 46

ctgcagggtt agcttcactt tcagttgctt atagaagcac aattctactt atatcgtgcg      60
atcccgctct gagttccgac ggggcggga ataaccgaag actacaacga agattattat      120
aattaacacg acgaacgcac taatcagaat cagcgggttg ccggagctct tgccgctgct      180
gttaccgcgtc ctcccactga ccgaaccgcc tacagcgtca actaaatctg ctagccccgag      240
gtcggccacc agtcgtccca acgtacccgg ctaaacgcag taaaatgttag cgttttctgg      300
cagtgtacgt gcgtctaaaa atttgttggct ggacggctcg gccaacacgt ccgttggcg      360
gcaaacactt cgttctacac ttttattata accgctgcaa atggcttggg cctcccaac      420
gctatcgtaa atggggtcac ccgattcgcc cggaaaaacc tcctccaacg aaaccacaga      480
cggatccata ccgcaggata tccaaagtaa ataatggcgc accacccgaaac cgtccgcctc      540
acgttgttca ataaaacgcac caccatacgt attcaaataat tggtagagct cggccgcgag      600
cagagccccca cctacaattt caagtgaaac acctgcaccc ttgatcagc caccggccgt      660
aagccggtca cgtagcctcg g atg acg cgc aag tgc atc cgt aat ttc ctg      711
Met Thr Arg Lys Cys Ile Arg Asn Phe Leu
    1           5           10

ctc ggt tct cgc gtt ggc caa gtt cgg atc cct aac gcg aat tgc ggc      759
Leu Gly Ser Arg Val Gly Gln Val Arg Ile Pro Asn Ala Asn Cys Gly
    15          20          25

ctc gtc tgc gcg cac cgc ctg gta cag att atc ggg cag cga att gcc      807
Leu Val Cys Ala His Arg Leu Val Gln Ile Ile Gly Gln Arg Ile Ala
    30          35          40

ccg tat att gtt gag ccc agc ccg ctc gga cga ggt cat gcg caa cct      855
Pro Tyr Ile Val Glu Pro Ser Pro Leu Gly Arg Gly His Ala Gln Pro
    45          50          55

gtt gag cac ctg ttg gtc tcc acg tgc taaaccgggt tcaaattcac      902
Val Glu His Leu Leu Val Ser Thr Ser
    60          65

gcataaggcat agtcgggtcg tcggccgc taaccaagtg gggctcgtaa agttggtccc      962
catttcggga caccgtgggc acctcccgta ttggaggtc gaatatgcgc tgcag      1017

<210> SEQ ID NO 47
<211> LENGTH: 67

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<212> TYPE: PRT
<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 47

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Met Thr Arg Lys Cys Ile Arg Asn Phe Leu Leu Gly Ser Arg Val Gly
 1           5          10          15

Gln Val Arg Ile Pro Asn Ala Asn Cys Gly Leu Val Cys Ala His Arg
 20          25          30

Leu Val Gln Ile Ile Gly Gln Arg Ile Ala Pro Tyr Ile Val Glu Pro
 35          40          45

Ser Pro Leu Gly Arg Gly His Ala Gln Pro Val Glu His Leu Leu Val
 50          55          60

Ser Thr Ser
 65

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<210> SEQ ID NO 48
<211> LENGTH: 1076
<212> TYPE: DNA
<213> ORGANISM: mosquito baculovirus
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)...(1071)

<400> SEQUENCE: 48

ctg cag ccc cgg gtc cag ccc aag ccg cag aag gag cgt att gtc gtg	48
Leu Gln Pro Arg Val Gln Pro Lys Pro Gln Lys Glu Arg Ile Val Val	
1 5 10 15	
gtg act tcg gtc acc aaa atc acc gcc gac gag gat gat gtc gat ggt	96
Val Thr Ser Val Thr Lys Ile Thr Ala Asp Glu Asp Asp Val Asp Gly	
20 25 30	
gag cag aag gtt acc ttt cgc gag ggt gaa aaa act tcg tgg gcc ttt	144
Glu Gln Lys Val Thr Phe Arg Glu Gly Glu Lys Thr Ser Trp Ala Phe	
35 40 45	
tac gac caa ccg gag gaa ctg gag gtt aat ggc gct tac tcg gtg gtg	192
Tyr Asp Gln Pro Glu Glu Leu Glu Val Asn Gly Ala Tyr Ser Val Val	
50 55 60	
atc aaa acc gag cgc aac aac ttt atg atg gtg aac cgt atc gtg gag	240
Ile Lys Thr Glu Arg Asn Asn Phe Met Met Val Asn Arg Ile Val Glu	
65 70 75 80	
gcg aaa aag tcc act att gtc gaa aac agg tac gtt tca ccg ttt gta	288
Ala Lys Lys Ser Thr Ile Val Glu Asn Arg Tyr Val Ser Pro Phe Val	
85 90 95	
gag aaa att gcg atg ggt aat ttg ctc ggt cgc gtt gtg cac ttt acg	336
Glu Lys Ile Ala Met Gly Asn Leu Leu Gly Arg Val Val His Phe Thr	
100 105 110	
tac tcg ggc agg gag aaa acg ttc atg atg tta ctg gaa gtt ttg act	384
Tyr Ser Gly Arg Asp Lys Thr Phe Met Met Leu Leu Glu Val Leu Thr	
115 120 125	
ctc gat gtg aac gta tgt acg gtg gag gtt cga gtg cag cgg gaa ttt	432
Leu Asp Val Asn Val Cys Thr Val Glu Val Arg Val Gln Arg Glu Phe	
130 135 140	
gaa tcg gag cac aat ttg atg caa gtt gtg cac gac ccg gcc aag tcc	480
Glu Ser Glu His Asn Leu Met Gln Val Val His Asp Arg Ala Lys Ser	
145 150 155 160	
agg ctc aac tgg acc gtg ttg tat gat gtg cgc gta aat tca ccg agt	528
Arg Leu Asn Trp Thr Val Leu Tyr Asp Val Arg Val Asn Ser Arg Ser	
165 170 175	
tac cgc ttt gag cgc atc gat gag acg aga aat tta acc acc gta tac	576
Tyr Arg Phe Glu Arg Ile Asp Glu Thr Arg Asn Leu Thr Thr Val Tyr	
180 185 190	

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atg ttg tct acg agc aac atc aag ttc tac gac acc ctg aac gac ctg Met Leu Ser Thr Ser Asn Ile Lys Phe Tyr Asp Thr Leu Asn Asp Leu 195 200 205	624
ctc gag gcc aac acg tgc acg ctt acg tcg aag gag cag acg ctt ttg Leu Glu Ala Asn Thr Cys Thr Leu Ser Ser Lys Glu Gln Thr Leu Leu 210 215 220	672
acg aag gct aca ttt acc cct ctt aaa ttt cat tcc ctc acc cgc gga Thr Lys Ala Thr Phe Thr Pro Leu Lys Phe His Ser Leu Thr Arg Gly 225 230 235 240	720
tac gac ctg cac atc ttc aac gtc aag caa gta aag gtg ttc ctc acc Tyr Asp Leu His Ile Phe Asn Val Lys Gln Val Lys Val Phe Leu Thr 245 250 255	768
gag gag ggc ggc atc atg agg ggc atc tgt tcc ttc ccg tac gcc aaa Glu Glu Gly Ile Met Arg Gly Ile Cys Ser Phe Pro Tyr Ala Lys 260 265 270	816
cgc cag tgg tca ctg tcc atc tat aac aac gaa aag aat cca aac gtt Arg Gln Trp Ser Leu Ser Ile Tyr Asn Asn Glu Lys Asn Pro Asn Val 275 280 285	864
ttc aaa aac tac atc gag cgg cta agc gac tac acc tcc acc gaa aac Phe Lys Asn Tyr Ile Glu Arg Leu Ser Asp Tyr Thr Ser Thr Glu Asn 290 295 300	912
agc tac ttc aac gtt tac ttc aac gac acc ggc tcc tcg tac acc ttc Ser Tyr Phe Asn Val Tyr Phe Asn Asp Thr Gly Ser Ser Tyr Thr Phe 305 310 315 320	960
att gcc att tcg ggc cgc tac gaa agt tca gag gaa tcg ttt tgc acc Ile Ala Ile Ser Gly Arg Tyr Glu Ser Ser Glu Glu Ser Phe Cys Thr 325 330 335	1008
gtt atg aat cca cca ccg gag gag cgt aag gtc gct gtc aag cgc ccc Val Met Asn Pro Pro Glu Glu Arg Lys Val Ala Val Lys Arg Pro 340 345 350	1056
atc gtt gat gac aac tgccag Ile Val Asp Asp Asn 355	1076

<210> SEQ ID NO 49
<211> LENGTH: 357
<212> TYPE: PRT
<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 49

Leu Gln Pro Arg Val Gln Pro Lys Pro Gln Lys Glu Arg Ile Val Val 1 5 10 15
Val Thr Ser Val Thr Lys Ile Thr Ala Asp Glu Asp Asp Val Asp Gly 20 25 30
Glu Gln Lys Val Thr Phe Arg Glu Gly Glu Lys Thr Ser Trp Ala Phe 35 40 45
Tyr Asp Gln Pro Glu Glu Leu Glu Val Asn Gly Ala Tyr Ser Val Val 50 55 60
Ile Lys Thr Glu Arg Asn Asn Phe Met Met Val Asn Arg Ile Val Glu 65 70 75 80
Ala Lys Lys Ser Thr Ile Val Glu Asn Arg Tyr Val Ser Pro Phe Val 85 90 95
Glu Lys Ile Ala Met Gly Asn Leu Leu Gly Arg Val Val His Phe Thr 100 105 110
Tyr Ser Gly Arg Asp Lys Thr Phe Met Met Leu Leu Glu Val Leu Thr 115 120 125
Leu Asp Val Asn Val Cys Thr Val Glu Val Arg Val Gln Arg Glu Phe 130 135 140

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Glu Ser Glu His Asn Leu Met Gln Val Val His Asp Arg Ala Lys Ser
 145 150 155 160

Arg Leu Asn Trp Thr Val Leu Tyr Asp Val Arg Val Asn Ser Arg Ser
 165 170 175

Tyr Arg Phe Glu Arg Ile Asp Glu Thr Arg Asn Leu Thr Thr Val Tyr
 180 185 190

Met Leu Ser Thr Ser Asn Ile Lys Phe Tyr Asp Thr Leu Asn Asp Leu
 195 200 205

Leu Glu Ala Asn Thr Cys Thr Leu Ser Ser Lys Glu Gln Thr Leu Leu
 210 215 220

Thr Lys Ala Thr Phe Thr Pro Leu Lys Phe His Ser Leu Thr Arg Gly
 225 230 235 240

Tyr Asp Leu His Ile Phe Asn Val Lys Gln Val Lys Val Phe Leu Thr
 245 250 255

Glu Glu Gly Ile Met Arg Gly Ile Cys Ser Phe Pro Tyr Ala Lys
 260 265 270

Arg Gln Trp Ser Leu Ser Ile Tyr Asn Asn Glu Lys Asn Pro Asn Val
 275 280 285

Phe Lys Asn Tyr Ile Glu Arg Leu Ser Asp Tyr Thr Ser Thr Glu Asn
 290 295 300

Ser Tyr Phe Asn Val Tyr Phe Asn Asp Thr Gly Ser Ser Tyr Thr Phe
 305 310 315 320

Ile Ala Ile Ser Gly Arg Tyr Glu Ser Ser Glu Glu Ser Phe Cys Thr
 325 330 335

Val Met Asn Pro Pro Pro Glu Glu Arg Lys Val Ala Val Lys Arg Pro
 340 345 350

Ile Val Asp Asp Asn
 355

<210> SEQ ID NO 50
 <211> LENGTH: 1076
 <212> TYPE: DNA
 <213> ORGANISM: mosquito baculovirus
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (715)...(894)
 <221> NAME/KEY: CDS
 <222> LOCATION: (927)...(1076)

<400> SEQUENCE: 50

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ctgcagttgt catcaacgat gggcgcttg acagcgacct tacgctccctc cgggtgggtaa 60
ttcataacgg tgcaaacgaa ttccctctgaa ctccgttgc ggcccgaaat ggcaatgaag 120
gtgtacgagg agccgggtgtc gttgaagttaa acgttgaagt agctgttttc ggtggagggtg 180
tagtcgctta gcccgtcgtat gtatgttttg aaaacgttttgc gattcttttc gttgttata 240
atggacagtg accactggcg tttggcgtaa gggaaaggaaac agatgcccct catgatgccg 300
ccctccctcg tgaggaaacac ctttacttgc ttgacgttgc agatgtgcag gtcgtatccg 360
cgggtgaggaa aatgaaattt aagaggggta aatgttagcct tcgtcaaaag cgtctgtcc 420
ttcgagctaa gcgtcacgt gttggcctcg agcaggtcgt tcagggtgtc ttagaaacttg 480
atgttgcgtc tagacaacat gtatacggtg gttaaatttc tcgtctcatc gatgcgtca 540
aagcggtaac tgcgtgaatt tacgcgcaca tcataacaaca cggtccagg tggcctggac 600
ttggcccggt cgtgcacaac ttgcataaaa ttgtgtccg attcaaattc ccgctgcact 660
cgaacctcca ccgtacatac gttcacatcg agagtcaaaa cttccagtaa catc atg 717
Met
  
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1

aac gtt ttg tcc ctg ccc gag tac gta aag tgc aca acg cga ccg agc 765
 Asn Val Leu Ser Leu Pro Glu Tyr Val Lys Cys Thr Thr Arg Pro Ser
 5 15

aaa tta ccc atc gca att ttc tct aca aac ggt gaa acg tac ctg ttt 813
 Lys Leu Pro Ile Ala Ile Phe Ser Thr Asn Gly Glu Thr Tyr Leu Phe
 20 25 30

tcg aca ata gtg gac ttt ttc gcc tcc acg ata cgg ttc acc atc ata 861
 Ser Thr Ile Val Asp Phe Ala Ser Thr Ile Arg Phe Thr Ile Ile
 35 40 45

aag ttg ttg cgc tcg gtt ttg atc acc acc gag taagcgccat taacctccag 914
 Lys Leu Leu Arg Ser Val Leu Ile Thr Thr Glu
 50 55 60

ttcctccgt tg gtc gta aaa ggc cca cga agt ttt ttc acc ctc gcg aaa 965
 Val Val Lys Gly Pro Arg Ser Phe Phe Thr Leu Ala Lys
 65 70

ggt aac ctt ctg ctc acc atc gac atc atc ctc gtc ggc ggt gat ttt 1013
 Gly Asn Leu Leu Leu Thr Ile Asp Ile Ile Leu Val Gly Gly Asp Phe
 75 80 85

ggt gac cga agt cac cac gac aat acg ctc ctt ctg cgg ctt ggg ctg 1061
 Gly Asp Arg Ser His His Asp Asn Thr Leu Leu Arg Leu Gly Leu
 90 95 100 105

gac ccg ggg ctg cag 1076
 Asp Pro Gly Leu Gln
 110

<210> SEQ ID NO 51

<211> LENGTH: 60

<212> TYPE: PRT

<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 51

Met Asn Val Leu Ser Leu Pro Glu Tyr Val Lys Cys Thr Thr Arg Pro
 1 5 10 15

Ser Lys Leu Pro Ile Ala Ile Phe Ser Thr Asn Gly Glu Thr Tyr Leu
 20 25 30

Phe Ser Thr Ile Val Asp Phe Phe Ala Ser Thr Ile Arg Phe Thr Ile
 35 40 45

Ile Lys Leu Leu Arg Ser Val Leu Ile Thr Thr Glu
 50 55 60

<210> SEQ ID NO 52

<211> LENGTH: 50

<212> TYPE: PRT

<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 52

Val Val Lys Gly Pro Arg Ser Phe Phe Thr Leu Ala Lys Gly Asn Leu
 1 5 10 15

Leu Leu Thr Ile Asp Ile Ile Leu Val Gly Gly Asp Phe Gly Asp Arg
 20 25 30

Ser His His Asp Asn Thr Leu Leu Leu Arg Leu Gly Leu Asp Pro Gly
 35 40 45

Leu Gln
 50

<210> SEQ ID NO 53

<211> LENGTH: 1656

<212> TYPE: DNA

<213> ORGANISM: mosquito baculovirus

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<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (434)...(1656)
<221> NAME/KEY: CDS
<222> LOCATION: (94)...(252)

<400> SEQUENCE: 53

ctgcaggtga agcgatagg ttagctggc agaagttatc tgtacattgc ccaggaggag      60
gttcaatta cggcccggtg cactaatcgc acc atg att cgt cag ctt acg ggc      114
                                         Met Ile Arg Gln Leu Thr Gly
                                         1           5

gtc ggt atc gtc aca gct gac agt ggc tgc agc cga acc cgg cgc cgt      162
Val Gly Ile Val Thr Ala Asp Ser Gly Cys Ser Arg Thr Arg Arg Arg
 10          15           20

aaa tgg cgc acg gcc cgc acg gca gct acg ccc cgg cgg gcc gca ccc      210
Lys Trp Arg Thr Ala Arg Thr Ala Ala Thr Pro Arg Arg Ala Ala Pro
 25          30           35

gct gct cat cgc tgc gcc gtc gtt tct tgc gtt acc gca tct      252
Ala Ala His Arg Cys Ala Val Val Ser Cys Val Thr Ala Ser
 40          45           50

tgagccgcgt gcgcgcgacg aacaacgcgg caaggcttag caccgcgcag cccatcatcgat      312
aaagcgcggg cgacagccgg ttgcgcgtcg cgctgatcg ccaggtgatcg acgaacggcg      372
cgaaggcgcc gaacagcgtg acacccgtgt ttagctgac cgcgagcccc gtagcgcgcg      432
t ctg cga cgg gaa cag ctc ggc cat cag cgc cgg cag cgc gcc gca gta      481
Leu Arg Arg Glu Gln Leu Gly His Gln Arg Arg Gln Arg Ala Ala Val
 55          60           65

cat cgc cttcaa tgc gcc gat cca gac cag cgc cgc gag cat cgt cgc      529
His Arg Leu Gln Cys Ala Asp Pro Asp Gln Arg Arg Glu His Arg Arg
 70          75           80           85

gaa cga tgc gtg acg cgt gag cca ctc gaa cgt cgg gta cac ggt gac      577
Glu Arg Cys Val Thr Arg Glu Pro Leu Glu Arg Arg Val His Gly Asp
 90          95           100

gag cat cag gac cgc gac cgc cat cat gct gat ccc ggg gct gct      625
Glu His Gln Asp Arg Arg Asp Arg His His Ala Asp Pro Pro Gly Ala
105          110           115

atc gga cag gtg gcc gac gat cgg cgt gac gag cgt gag cac gaa gcc      673
Ile Gly Gln Val Ala Asp Asp Arg Arg Asp Glu Arg His Glu Ala
120          125           130

ggc cgc gag cgt cgc gac acc cgt cga cgc ggg cag ccc gag ctg      721
Gly Arg Glu Arg Arg Glu Thr Arg Arg Gly Gln Pro Glu Leu
135          140           145

ctt gat cgc gta agt cgg cat gta cag gat cat gta gtt gat cgc ggt      769
Leu Asp Arg Val Ser Arg His Val Gln Asp His Val Val Asp Arg Gly
150          155           160           165

cga gat cac gag cgc gcc gat cga cag cag cac ccg cac ctt ttg ttc      817
Arg Asp His Glu Arg Ala Asp Arg Gln Gln His Pro His Leu Leu Phe
170          175           180

cgc gaa cag ctc gct cac cgg cgc ttc gga gct tgc cgt ctt gaa      865
Arg Glu Gln Leu Ala His Arg Arg Phe Gly Ala Cys Leu Arg Leu Glu
185          190           195

ttc aac gcc ttc gtc gac gta acg gct gat gta cag ccc gac cgg gcc      913
Phe Asn Ala Phe Val Asp Val Thr Ala Asp Val Gln Pro Asp Arg Ala
200          205           210

gat cgc gag ccc gaa cag gaa cgg cac gct cca gcc cca gct ttc gag      961
Asp Arg Glu Pro Glu Gln Glu Arg His Ala Pro Ala Pro Ala Phe Glu
215          220           225

ttg cgc agg cgt cag cgt gga tgt cag cag cgc acc gaa gcc cga tgc      1009
Leu Arg Arg Arg Gln Arg Gly Cys Gln Gln Arg Thr Glu Ala Arg Cys
230          235           240           245

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gag cag cgt cgc gag gcc ctg gct cgc gaa ctg cca gct cga cat gaa Glu Gln Arg Arg Glu Ala Leu Ala Arg Glu Leu Pro Ala Arg His Glu 250 255 260	1057
acc gcg ccg ctg cgg cgc gtg ctc gac gag gaa cgc ggt cga gct cgc Thr Ala Pro Leu Arg Arg Val Leu Asp Glu Glu Arg Gly Arg Ala Arg 265 270 275	1105
gaa ttc gcc gcc cgc gga aaa gcc ctg cat caa ccc cga cag cat gat Glu Phe Ala Ala Arg Gly Lys Ala Leu His Gln Pro Arg Gln His Asp 280 285 290	1153
ccc gag cgg tgc gag tat gcc gat cga tgc gta ggt cgg cat cag cgc Pro Glu Arg Cys Glu Tyr Ala Asp Arg Cys Val Gly Arg His Gln Arg 295 300 305	1201
gat cag cag cgt gcc ggc cat cat cat cgc gat cga cag cag cga Asp Gln Gln Arg Ala Gly His His Arg Asp Arg Gln Gln Gln Arg 310 315 320 325	1249
cgc ctt gcc cgc tcg atc ggc gta tgc gcc gag cac gaa gcc gcc Arg Leu Ala Ala Arg Ser Ile Gly Val Cys Ala Glu His Glu Ala Ala 330 335 340	1297
gat cgg ccc gat cag gta gga cag ccc gaa cgt gcc gag cgt gag cat Asp Arg Pro Asp Gln Val Gly Gln Pro Glu Arg Ala Glu Arg Glu His 345 350 355	1345
cag cga tgt cgc ttc gct cgt ggc ggg gaa gaa cag ctt ggc gat cgt Gln Arg Cys Arg Phe Ala Arg Gly Gly Glu Glu Gln Leu Gly Asp Arg 360 365 370	1393
cac cgc gaa gaa gcc gta gac gat cag gtc gaa cca ttc gag cgc gtt His Arg Glu Glu Ala Val Asp Asp Gln Val Glu Pro Phe Glu Arg Val 375 380 385	1441
gcc gat cga cgc cgc gaa gat gat gct cgc gat ctt cgc ggc gct ggg Ala Asp Arg Arg Arg Asp Asp Ala Pro Asp Leu Arg Gly Ala Gly 390 395 400 405	1489
gcg ggc ggc ttc gtg cga ggt cag ggt ggt cgt att cat cgc gta tgc Ala Gly Gly Phe Val Arg Gly Gln Gly Arg Ile His Arg Val Cys 410 415 420	1537
agg tcc cgt gaa agg ggc gaa gcg cgt tac agg ggc gcg ccg gcc gcg Arg Ser Arg Glu Arg Gly Glu Ala Arg Tyr Arg Ala Ala Pro Ala Ala 425 430 435	1585
gcg ggc gcc gcg tgg cga acg gtc ggc gcg tcg tcg ccg aga tcc cag Ala Gly Ala Ala Trp Arg Thr Val Gly Ala Ser Ser Pro Arg Ser Gln 440 445 450	1633
aag agg ccg gcc atc atc tgc ag Lys Arg Pro Ala Ile Ile Cys 455 460	1656

<210> SEQ ID NO 54
<211> LENGTH: 53
<212> TYPE: PRT
<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 54

Met Ile Arg Gln Leu Thr Gly Val Gly Ile Val Thr Ala Asp Ser Gly 1 5 10 15
Cys Ser Arg Thr Arg Arg Lys Trp Arg Thr Ala Arg Thr Ala Ala 20 25 30
Thr Pro Arg Arg Ala Ala Pro Ala Ala His Arg Cys Ala Val Val Ser 35 40 45
Cys Val Thr Ala Ser 50

<210> SEQ ID NO 55

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<211> LENGTH: 407
<212> TYPE: PRT
<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 55

Leu Arg Arg Glu Gln Leu Gly His Gln Arg Arg Gln Arg Ala Ala Val
 1           5          10          15

His Arg Leu Gln Cys Ala Asp Pro Asp Gln Arg Arg Glu His Arg Arg
 20          25          30

Glu Arg Cys Val Thr Arg Glu Pro Leu Glu Arg Arg Val His Gly Asp
 35          40          45

Glu His Gln Asp Arg Arg Asp Arg His His Ala Asp Pro Pro Gly Ala
 50          55          60

Ile Gly Gln Val Ala Asp Asp Arg Arg Asp Glu Arg Glu His Glu Ala
 65          70          75          80

Gly Arg Glu Arg Arg Glu Thr Arg Arg Gly Gln Pro Glu Leu
 85          90          95

Leu Asp Arg Val Ser Arg His Val Gln Asp His Val Val Asp Arg Gly
100          105          110

Arg Asp His Glu Arg Ala Asp Arg Gln Gln His Pro His Leu Leu Phe
115          120          125

Arg Glu Gln Leu Ala His Arg Arg Phe Gly Ala Cys Leu Arg Leu Glu
130          135          140

Phe Asn Ala Phe Val Asp Val Thr Ala Asp Val Gln Pro Asp Arg Ala
145          150          155          160

Asp Arg Glu Pro Glu Gln Glu Arg His Ala Pro Ala Pro Ala Phe Glu
165          170          175

Leu Arg Arg Arg Gln Arg Gly Cys Gln Gln Arg Thr Glu Ala Arg Cys
180          185          190

Glu Gln Arg Arg Glu Ala Leu Ala Arg Glu Leu Pro Ala Arg His Glu
195          200          205

Thr Ala Pro Leu Arg Arg Val Leu Asp Glu Glu Arg Gly Arg Ala Arg
210          215          220

Glu Phe Ala Ala Arg Gly Lys Ala Leu His Gln Pro Arg Gln His Asp
225          230          235          240

Pro Glu Arg Cys Glu Tyr Ala Asp Arg Cys Val Gly Arg His Gln Arg
245          250          255

Asp Gln Gln Arg Ala Gly His His His Arg Asp Arg Gln Gln Gln Arg
260          265          270

Arg Leu Ala Ala Arg Ser Ile Gly Val Cys Ala Glu His Glu Ala Ala
275          280          285

Asp Arg Pro Asp Gln Val Gly Gln Pro Glu Arg Ala Glu Arg Glu His
290          295          300

Gln Arg Cys Arg Phe Ala Arg Gly Gly Glu Gln Leu Gly Asp Arg
305          310          315          320

His Arg Glu Glu Ala Val Asp Asp Gln Val Glu Pro Phe Glu Arg Val
325          330          335

Ala Asp Arg Arg Glu Asp Asp Ala Pro Asp Leu Arg Gly Ala Gly
340          345          350

Ala Gly Gly Phe Val Arg Gly Gln Gly Gly Arg Ile His Arg Val Cys
355          360          365

Arg Ser Arg Glu Arg Gly Glu Ala Arg Tyr Arg Ala Ala Pro Ala Ala
370          375          380

Ala Gly Ala Ala Trp Arg Thr Val Gly Ala Ser Ser Pro Arg Ser Gln

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385	390	395	400
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Lys Arg Pro Ala Ile Ile Cys
405

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<210> SEQ_ID NO 56
<211> LENGTH: 1656
<212> TYPE: DNA
<213> ORGANISM: mosquito baculovirus
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (894)...(1184)
<221> NAME/KEY: CDS
<222> LOCATION: (1440)...(1656)

<400> SEQUENCE: 56

ctgcaggta agcggatagg tgagctggc agaagttatc tgtacattgc ccaggaggag      60
gttcaatta cggcccggtt cactaatcgc accatgattc gtcagcttac gggcggtcggt     120
atcgtcacag cggacagtgg ctgcagccga accccggcgcc gtaaatggcg cacggcccgc    180
acggcagcga cgcccgccgc ggccgcaccg gcccgcacatc gctgcgccgt cgtttcttgc    240
gttaccgcat cttgagccgc gtgcgcgcga cgaacaacgc ggcaggctc agcaccgcgc    300
agccccatcag ataaaagcgcg ggcgacagcc gtttgccgt cgcgctgatc agccaggta     360
tgacgaacgg cgcgaagccg cgcgaaacagcg tgacacccgt gtttagctg accgcgagcc    420
ccgttagcgcg cgtctgcgc acggaaacatcag cgcgcgcgcg cgcgcgcgact            480
acatcgccctt caatgcgcgcg atccagacca gcgcgcgcg catcgatcgcg aacgatgcgt   540
gacgcgtgag ccactcgaac gtccggatac cggtagcgcg catcaggacc gccgcgaccg    600
ccatcatcgcg gatccgcgcg gtgcgcgcg acaggatggcc gacgatcgcg gtgacgagcg    660
tgagcacgaa gcccgtcgcg agcgtcgcgc cggaaacccgt cgcgcggccg agcccgagct   720
gcttgatcgc gtaagtccgc atgtacagga tcatgttagtt gatcgcggc gagatcacga    780
gcgcgcgcgat cgacagcgc accccgcacatc tttgtccgc gAACAGCTCG CGCACCGGGCG 840
cttcggagcg tgcctcgatc ttgaattcaa cgccttcgcg gacgtaacgg cgg atg          896
                                         Met
                                         1

tac agc ccg acc ggg ccg atc gcg agc ccg aac agg aac ggc acg cgc      944
Tyr Ser Pro Thr Gly Pro Ile Ala Ser Pro Asn Arg Asn Gly Thr Arg
  5           10           15

cag ccc cag ctt tcg agt tgc gca ggc gtc agc gtg gat gtc agc agc      992
Gln Pro Gln Leu Ser Ser Cys Ala Gly Val Ser Val Asp Val Ser Ser
  20          25           30

gca ccg aag ccc gat gcg agc agc gtc gcg agg ccc tgg ctc gcg aac      1040
Ala Pro Lys Pro Asp Ala Ser Ser Val Ala Arg Pro Trp Leu Ala Asn
  35          40           45

tgc cag ctc gac atg aaa ccg cgc cgc tgc ggc gcg tgc tcg acg agg      1088
Cys Gln Leu Asp Met Lys Pro Arg Arg Cys Gly Ala Cys Ser Thr Arg
  50          55           60           65

aac gcg gtc gag ctc gcg aat tcg ccg ccc gcg gaa aag ccc tgc atc      1136
Asn Ala Val Glu Leu Ala Asn Ser Pro Pro Ala Glu Lys Pro Cys Ile
  70          75           80

aac cgc gac atg atc ccg agc ggt gcg agt atg ccg atc gat gcg      1184
Asn Arg Asp Ser Met Ile Pro Ser Gly Ala Ser Met Pro Ile Asp Ala
  85          90           95

taggtcgca tcagcgcgat cagcagcgtg cggccatca tcatcgatc cgcacagcgc      1244
agcgacgcct tgcggccgcg tcgatcgccg tatgcgcgcg gacgaaagcc gcccgcgc      1304
cggatcaggta aggacagccc gaaacgtgccc agcgtgagca tcagcgtatc cgcttcgcgc 1364

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gtggcgggga agaacagctt ggcgatcgac accgcagaaga agccgttagac gatcaggatcg	1424
aaccattcga gcgcg ttg ccg atc gac gcc gcg aag atg atg cgc cgg atc Leu Pro Ile Asp Ala Ala Lys Met Met Arg Arg Ile 100 105	1475
ttc gcg gcg ctg ggg cgg gcg gct tcg tgc gag gtc agg gtg gtc gta Phe Ala Ala Leu Gly Arg Ala Ala Ser Cys Glu Val Arg Val Val Val 110 115 120 125	1523
ttc atc gcg tat gca ggt ccc gtc aaa ggg gcg aag cgc gtt aca ggg Phe Ile Ala Tyr Ala Gly Pro Val Lys Gly Ala Lys Arg Val Thr Gly 130 135 140	1571
cgg cgc cgg ccg cgg gcg ccg cgt ggc gaa cgg tcg gcg cgt cgt Arg Arg Arg Pro Arg Arg Ala Pro Arg Gly Glu Arg Ser Ala Arg Arg 145 150 155	1619
cgc cga gat ccc aga aga ggc cgg cca tca tot gca g Arg Arg Asp Pro Arg Arg Gly Arg Pro Ser Ser Ala 160 165	1656

<210> SEQ ID NO 57
<211> LENGTH: 97
<212> TYPE: PRT
<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 57

Met Tyr Ser Pro Thr Gly Pro Ile Ala Ser Pro Asn Arg Asn Gly Thr 1 5 10 15
Arg Gln Pro Gln Leu Ser Ser Cys Ala Gly Val Ser Val Asp Val Ser 20 25 30
Ser Ala Pro Lys Pro Asp Ala Ser Ser Val Ala Arg Pro Trp Leu Ala 35 40 45
Asn Cys Gln Leu Asp Met Lys Pro Arg Arg Cys Gly Ala Cys Ser Thr 50 55 60
Arg Asn Ala Val Glu Leu Ala Asn Ser Pro Pro Ala Glu Lys Pro Cys 65 70 75 80
Ile Asn Arg Asp Ser Met Ile Pro Ser Gly Ala Ser Met Pro Ile Asp 85 90 95

Ala

<210> SEQ ID NO 58
<211> LENGTH: 72
<212> TYPE: PRT
<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 58

Leu Pro Ile Asp Ala Ala Lys Met Met Arg Arg Ile Phe Ala Ala Leu 1 5 10 15
Gly Arg Ala Ala Ser Cys Glu Val Arg Val Val Val Phe Ile Ala Tyr 20 25 30
Ala Gly Pro Val Lys Gly Ala Lys Arg Val Thr Gly Arg Arg Arg Pro 35 40 45
Arg Arg Ala Pro Arg Gly Glu Arg Ser Ala Arg Arg Arg Asp Pro 50 55 60
Arg Arg Gly Arg Pro Ser Ser Ala 65 70

<210> SEQ ID NO 59
<211> LENGTH: 1656
<212> TYPE: DNA
<213> ORGANISM: mosquito baculovirus

-continued

<220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1180)...(1338)

<400> SEQUENCE: 59

ctgcaggtga	agcggatagg	ttagactggc	agaagttatc	tgtacattgc	ccaggaggag	60
gtttcaatta	cggcccgtt	cactaatcgc	accatgattc	gtcagcttac	ggcgctcggt	120
atcgtcacag	cggacagtgg	ctgcagccga	accggcgcc	gtaaatggcg	cacggcccc	180
acggcagcga	cggccggcg	ggccgcaccg	gcccgcac	gctgcgcgt	cgtttcttgc	240
gttaccgc	catcttgcgc	gtgcgcgc	cgaacaacgc	ggcaaggctc	agcaccgc	300
agcccatcag	ataaaagcgc	ggcgacagcc	ggttgccgt	cgcgctgatc	agccagggtga	360
tgacgaacgg	cgcgaagccg	ccgaacagcg	tgacacccgt	gttgtagctg	accgcgagcc	420
ccgttagcgc	cgtctgcac	gggaacagct	cggccatcg	cgccggcagc	gcgcgcag	480
acatccctt	caatgcgc	atccagacca	gcccgcgag	catcgctcg	aacgatgcgt	540
gacgcgtgag	ccactcgaac	gtcggtaca	cggtgacgag	catcaggacc	gccgcgacc	600
ccatcatgcg	gatccgc	gtgcgtatcg	acaggtggcc	gacgatcg	gtgacgagc	660
tgagcacgaa	gcccgtcgc	agcgctgc	cggaaacccgt	cgacgcggc	agcccggag	720
gtttatgcgc	gtaatgcgc	atgtacagga	tcatgtat	gtcgccgtc	gagatcacga	780
gcccgcgc	cgacgcgc	acccgcac	tttgcgc	gAACAGCTCG	cgccaccggc	840
cttcggagcg	tgcctgc	ttgaattcaa	cgccttc	gacgtaacgg	cggtatgtaca	900
gcccgcacc	gcccgtcgc	agcccgaaca	ggaacggcac	gcccgc	cagcttcga	960
gttgcgc	cgtcagcgt	gatgtcagca	gcccgc	gacgtgc	agcagcgtc	1020
cgaggccctg	gctcgcgaa	tgccagctcg	acatgaaacc	gcccgcgt	ggcgcgt	1080
cgacgaggaa	cgcggcgt	ctcgcaatt	cgcgc	ggaaaagccc	tgcataacc	1140
gacgacgc	gatccgc	ggtgcgagta	tgccgatcg	atg cgt	agg tcg gca	1194
				Met	Arg Arg Ser Ala	
				1	5	
tca	gca	tca	gca	gca	gca	1242
Ser	Ala	Arg	Ser	Ala	Ala	
				Cys	Arg Pro	
				Ser	Ser Ser	
				Arg	Arg Ser	
				Ser	Thr Arg	
				Thr	Ala	
10	15	20				
gca	gca	acg	cct	tgc	ggc	1290
Ala	Ala	Ala	Pro	Cys	Gly	
25	30	35				
agc	cgc	cga	tcg	gcc	gga	1338
Ser	Arg	Arg	Ser	Ala	Gly	
40	45	50				
tgagcatcag	cgtatgcgt	tgcgtcgt	cggggaa	cagcttgc	atcgtaacc	1398
cgaagaagcc	gtagacgatc	aggcgtac	attcgacgc	gttgcgc	gacgcgc	1458
agatgtatcg	ccggatcttc	gcccgcgt	ggcgccgc	tgcgtgc	gtcagggtgg	1518
tcgtattat	cgcgtatcg	gttccgt	aaggggcgaa	gcccgttaca	ggcgcgc	1578
ggccgcggcg	ggccgcgcgt	ggcgtac	cggcgcgt	tcgcgc	gagatccc	1638
gcccgcgc	atctgcag					1656

<210> SEQ ID NO 60

<211> LENGTH: 53

<212> TYPE: PRT

<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 60

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Met Arg Arg Ser Ala Ser Ala Arg Ser Ala Ala Cys Arg Pro Ser Ser
 1           5          10          15
Ser Arg Ser Thr Ala Ala Ala Thr Pro Cys Gly Pro Leu Asp Arg Arg
20          25          30
Met Arg Arg Ala Arg Ser Arg Arg Ser Ala Gly Ser Gly Arg Thr Ala
35          40          45
Arg Thr Cys Arg Ala
50

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<210> SEQ ID NO 61

<211> LENGTH: 1656

<212> TYPE: DNA

<213> ORGANISM: mosquito baculovirus

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (129)...(1412)

<400> SEQUENCE: 61

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ctgcagatga tggccggcct cttctggat ctccggcgacg acgcgcggac cgttcgccac      60
gcggcgccccg ccgcggccgg cgccgcctg taacgcgcctt cgccccccttc acgggacactg      120
catacgcg atg aat acg acc acc ctg acc tcg cac gaa gcc gcc cgc ccc      170
  Met Asn Thr Thr Thr Leu Thr Ser His Glu Ala Ala Arg Pro
  1           5          10
agc gcc aag atc cgg cgc atc atc ttc gcg gcg tcg atc ggc aac      218
  Ser Ala Ala Lys Ile Arg Arg Ile Ile Phe Ala Ala Ser Ile Gly Asn
  15          20          25          30
gcg ctc gaa tgg ttc gac ctg atc gtc tac ggc ttc ttc gcg gtg acg      266
  Ala Leu Glu Trp Phe Asp Leu Ile Val Tyr Gly Phe Phe Ala Val Thr
  35          40          45
atc gcc aag ctg ttc ccc gcc acg agc gaa ggc aca tcg ctg atg      314
  Ile Ala Lys Leu Phe Phe Pro Ala Thr Ser Glu Ala Thr Ser Leu Met
  50          55          60
ctc acg ctc ggc acg ttc ggg ctg tcc tac ctg atc cgg ccg atc ggc      362
  Leu Thr Leu Gly Thr Phe Gly Leu Ser Tyr Leu Ile Arg Pro Ile Gly
  65          70          75
ggc ttc gtg ctc ggc gca tac gcc gat cga gcg ggc cgc aag gcg tcg      410
  Gly Phe Val Leu Gly Ala Tyr Ala Asp Arg Ala Gly Arg Lys Ala Ser
  80          85          90
ctg ctg ctg atc gcg atg atg atg gcc ggc acg ctg ctg atc gcg      458
  Leu Leu Leu Ser Ile Ala Met Met Met Ala Gly Thr Leu Leu Ile Ala
  95          100         105         110
ctg atg ccg acc tac gca tcg atc ggc ata ctc gca ccg ctc ggg atc      506
  Leu Met Pro Thr Tyr Ala Ser Ile Gly Ile Leu Ala Pro Leu Gly Ile
  115         120         125
atg ctg tcg cgg ttg atg cag ggc ttt tcc gcg ggc ggc gaa ttc gcg      554
  Met Leu Ser Arg Leu Met Gln Gly Phe Ser Ala Gly Gly Glu Phe Ala
  130         135         140
agc tcg acc gcg ttc ctc gtc gag cac gcg ccg cag cgg cgc ggt ttc      602
  Ser Ser Thr Ala Phe Leu Val Glu His Ala Pro Gln Arg Arg Gly Phe
  145         150         155
atg tcg agc tgg cag ttc gcg agc cag ggc ctc gcg acg ctg ctc gca      650
  Met Ser Ser Trp Gln Phe Ala Ser Gln Gly Leu Ala Thr Leu Leu Ala
  160         165         170
tcg ggc ttc ggt gcg ctg ctg aca tcc acg ctg acg cct gcg caa ctc      698
  Ser Gly Phe Gly Ala Leu Leu Thr Ser Thr Leu Thr Pro Ala Gln Leu
  175         180         185         190
gaa agc tgg ggc tgg cgc gtg ccg ttc ctg ttc ggg ctc gcg atc ggc      746
  Glu Ser Trp Gly Trp Arg Val Pro Phe Leu Phe Gly Leu Ala Ile Gly
  195         200         205

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cgc gtc ggg ctg tac atc cgc cgt tac gtc gac gaa ggc gtt gaa ttc Pro Val Gly Leu Tyr Ile Arg Arg Tyr Val Asp Glu Gly Val Glu Phe 210 215 220	794
aag acg cag gca cgc tcc gaa gcg ccg gtg cgc gag ctg ttc gcg gaa Lys Thr Gln Ala Arg Ser Glu Ala Pro Val Arg Glu Leu Phe Ala Glu 225 230 235	842
caa aag gtg cgg gtg ctg ctg tcg atc ggc gcg ctc gtg atc tcg acc Gln Lys Val Arg Val Leu Leu Ser Ile Gly Ala Leu Val Ile Ser Thr 240 245 250	890
gcg atc aac tac atg atc ctg tac atg ccg act tac gcg atc aag cag Ala Ile Asn Tyr Met Ile Leu Tyr Met Pro Thr Tyr Ala Ile Lys Gln 255 260 265 270	938
ctc ggg ctg ccc gcg tcg acg ggt ttc gcg gcg acg ctc gcg acc ggc Leu Gly Leu Pro Ala Ser Thr Gly Phe Ala Ala Thr Leu Ala Thr Gly 275 280 285	986
ttc gtg ctc acg ctc gtc acg ccg atc gtc ggc cac ctg tcc gat cgc Phe Val Leu Thr Leu Val Thr Pro Ile Val Gly His Leu Ser Asp Arg 290 295 300	1034
acc ggg cgg atc cgc atg atg gcg gtc gcg gcg gtc ctg atg ctc gtc Thr Gly Arg Ile Arg Met Met Ala Val Ala Ala Val Leu Met Leu Val 305 310 315	1082
acc gtg tac ccc acg ttc gag tgg ctc acg cgt cac gca tcg ttc gcg Thr Val Tyr Pro Thr Phe Glu Trp Leu Thr Arg His Ala Ser Phe Ala 320 325 330	1130
acg atg ctc gcg gcg ctg gtc tgg atc ggc gca ttg aag gcg atg tac Thr Met Leu Ala Ala Leu Val Trp Ile Gly Ala Leu Lys Ala Met Tyr 335 340 345 350	1178
tgc ggc gcg ctg ccc gcg ctg atg gcc gag ctg ttc ccg tcg cag acg Cys Gly Ala Leu Pro Ala Leu Met Ala Glu Leu Phe Pro Ser Gln Thr 355 360 365	1226
cgc gct acg ggg ctc gcg gtc agc tac aac acg ggt gtc acg ctg ttc Arg Ala Thr Gly Leu Ala Val Ser Tyr Asn Thr Gly Val Thr Leu Phe 370 375 380	1274
ggc ggc ttc gcg ccg ttc gtc atc acc tgg ctg atc acg gcg acc ggc Gly Gly Phe Ala Pro Phe Val Ile Thr Trp Leu Ile Ser Ala Thr Gly 385 390 395	1322
aac cgg ctg tcg ccc gcg ctt tat ctg atg ggc tgc gcg gtg ctg acg Asn Arg Leu Ser Pro Ala Leu Tyr Leu Met Gly Cys Ala Val Leu Ser 400 405 410	1370
ctt gcc gcg ttg ttc gtc gcg cgc acg cgg ctc aag atg cgg Leu Ala Ala Leu Phe Val Ala Arg Thr Arg Leu Lys Met Arg 415 420 425	1412
taacgcaga aacgacggcg cagcgatgcg ccggccggtc ggccccccgc ggcgtcgctg ccgtgcggc cgtgcgccat ttacggcgcc gggttcggt gcagccactg tccgctgtga	1472
cgataccgac gccccgtaaac tgacaaatca tggtgccatt agtgtcaacgg gcccgtatt aaacaccttc ctgggcaatg tacagataac ttctgccccag ctcacccatc cgcttcaccc	1532
gcag	1592
	1652

<211> LENGTH: 428
<212> TYPE: PRT
<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 62

Ala Lys Ile Arg Arg Ile Ile Phe Ala Ala Ser Ile Gly Asn Ala Leu

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20	25	30
Glu Trp Phe Asp Leu Ile Val Tyr Gly Phe Phe Ala Val Thr Ile Ala		
35	40	45
Lys Leu Phe Phe Pro Ala Thr Ser Glu Ala Thr Ser Leu Met Leu Thr		
50	55	60
Leu Gly Thr Phe Gly Leu Ser Tyr Leu Ile Arg Pro Ile Gly Gly Phe		
65	70	75
Val Leu Gly Ala Tyr Ala Asp Arg Ala Gly Arg Lys Ala Ser Leu Leu		
85	90	95
Leu Ser Ile Ala Met Met Met Ala Gly Thr Leu Leu Ile Ala Leu Met		
100	105	110
Pro Thr Tyr Ala Ser Ile Gly Ile Leu Ala Pro Leu Gly Ile Met Leu		
115	120	125
Ser Arg Leu Met Gln Gly Phe Ser Ala Gly Gly Glu Phe Ala Ser Ser		
130	135	140
Thr Ala Phe Leu Val Glu His Ala Pro Gln Arg Arg Gly Phe Met Ser		
145	150	155
Ser Trp Gln Phe Ala Ser Gln Gly Leu Ala Thr Leu Leu Ala Ser Gly		
165	170	175
Phe Gly Ala Leu Leu Thr Ser Thr Leu Thr Pro Ala Gln Leu Glu Ser		
180	185	190
Trp Gly Trp Arg Val Pro Phe Leu Phe Gly Leu Ala Ile Gly Pro Val		
195	200	205
Gly Leu Tyr Ile Arg Arg Tyr Val Asp Glu Gly Val Glu Phe Lys Thr		
210	215	220
Gln Ala Arg Ser Glu Ala Pro Val Arg Glu Leu Phe Ala Glu Gln Lys		
225	230	235
Val Arg Val Leu Leu Ser Ile Gly Ala Leu Val Ile Ser Thr Ala Ile		
245	250	255
Asn Tyr Met Ile Leu Tyr Met Pro Thr Tyr Ala Ile Lys Gln Leu Gly		
260	265	270
Leu Pro Ala Ser Thr Gly Phe Ala Ala Thr Leu Ala Thr Gly Phe Val		
275	280	285
Leu Thr Leu Val Thr Pro Ile Val Gly His Leu Ser Asp Arg Thr Gly		
290	295	300
Arg Ile Arg Met Met Ala Val Ala Ala Val Leu Met Leu Val Thr Val		
305	310	315
Tyr Pro Thr Phe Glu Trp Leu Thr Arg His Ala Ser Phe Ala Thr Met		
325	330	335
Leu Ala Ala Leu Val Trp Ile Gly Ala Leu Lys Ala Met Tyr Cys Gly		
340	345	350
Ala Leu Pro Ala Leu Met Ala Glu Leu Phe Pro Ser Gln Thr Arg Ala		
355	360	365
Thr Gly Leu Ala Val Ser Tyr Asn Thr Gly Val Thr Leu Phe Gly Gly		
370	375	380
Phe Ala Pro Phe Val Ile Thr Trp Leu Ile Ser Ala Thr Gly Asn Arg		
385	390	395
Leu Ser Pro Ala Leu Tyr Leu Met Gly Cys Ala Val Leu Ser Leu Ala		
405	410	415
Ala Leu Phe Val Ala Arg Thr Arg Leu Lys Met Arg		
420	425	

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<211> LENGTH: 1656
<212> TYPE: DNA
<213> ORGANISM: mosquito baculovirus
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (227)....(787)
<221> NAME/KEY: CDS
<222> LOCATION: (1438)....(1590)

<400> SEQUENCE: 63

ctgcagatga tggccggcct cttctggat ctggcgacg acgcgccac cggtcgccac      60
gcggcgcccc ccgcggccgg cgccgcctg taacgcgtt cgcccttgc acgggacctg      120
catacgcgtt gaatacgtacc accctgaccc cgcacgaacgc cgccgcggcc agcgccgcga      180
agatccggcg catcatcttc gcggcggtcgta tcggcaacgc gctcgaaatg gtt cga      235
                                         Met Val Arg
                                         1

cct gat cgt cta cgg ctt ctt cgc ggt gac gat cgc caa gct gtt ctt      283
Pro Asp Arg Leu Arg Leu Arg Gly Asp Asp Arg Gln Ala Val Leu
   5          10          15

ccc cgc cac gag cga agc gac atc gct gat gct gct cac gct cggtt      331
Pro Arg His Glu Arg Ser Asp Ile Ala Asp Ala His Ala Arg His Val
  20         25         30         35

cggtt gtc cta cct gat ccg gcc gat ccg cgg ctt cgt gct ccggcgc      379
Arg Ala Val Leu Pro Asp Pro Ala Asp Arg Arg Leu Arg Ala Arg Arg
  40         45         50

ata cgc cga tcg agc ggg ccg caa ggc gtc gct gct gtc gat cgc      427
Ile Arg Arg Ser Ser Gly Pro Gln Gly Val Ala Ala Ala Val Asp Arg
  55         60         65

gat gat gat ggc cgg cac gct gct gat cgc gct gat gcc gac cta cgc      475
Asp Asp Asp Gly Arg His Ala Ala Asp Arg Ala Asp Ala Leu Arg
  70         75         80

atc gat ccg cat act cgc acc gct ccg gat cat gct gtc gcg gtt gat      523
Ile Asp Arg His Thr Arg Ala Arg Asp His Ala Val Ala Val Asp
  85         90         95

gcgtt ggg ctt ttc cgc ggg cgg cga att cgc gag ctc gac ccgc gtt cct      571
Ala Gly Leu Phe Arg Gly Arg Arg Ile Arg Glu Leu Asp Arg Val Pro
 100        105        110        115

cgt cga gca cgc gcc gca gcg ccgtt cat gtc gag ctg gca gtt      619
Arg Arg Ala Arg Ala Ala Ala Arg Phe His Val Glu Leu Ala Val
 120        125        130

cgc gag cca ggg cct cgc gac gct gct cgc atc ggg ctt ccgtt gtc gct      667
Arg Glu Pro Gly Pro Arg Asp Ala Ala Arg Ile Gly Leu Arg Cys Ala
 135        140        145

gct gac atc cac gct gac gcc tgc gca act cga aag ctg ggg ctg gcg      715
Ala Asp Ile His Ala Asp Ala Cys Ala Thr Arg Lys Leu Gly Leu Ala
 150        155        160

cgt gcc gtt cct gtt ccg gct cgc gat ccg ccc ggt ccg gct gta cat      763
Arg Ala Val Pro Val Arg Ala Arg Asp Arg Pro Gly Arg Ala Val His
 165        170        175

ccg ccg tta cgt cga cga agg cgt tgaattcaag acgcaggcac gctccgaagc      817
Pro Pro Leu Arg Arg Arg Arg
 180        185

gcgggtgcgc gagctgttcg cggaaacaaaa ggtgcgggtg ctgtgtcgta tcggcgccgt      877
cgtgatctcg accgcgtatca actacatgtat cctgtacatgc cgcacttacg cgtatcaagca      937
gctcggtcgcc cccgcgtcg cgggttcgc ggcacgcgc ggcacccgc tcgtgtcgc      997
gctcggtcaccg cccgtatcgatcg gccacctgtc cgcacgcacc gggcgatcc gcatgtatggc      1057
ggtcggggcg gtcctgtatgc tcgtacccgt gtatccgcacg ttccgagtggc tcacgcgtca      1117

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cgcacgttc	gcgacgtgc	tcgcggcgct	ggtctggatc	ggcgcatattga	aggcgatgtta	1177
ctgcggcgcg	ctgcggcgcc	tgtatggccga	gctgttcccg	tcgcagacgc	cgctacggg	1237
gctcgccgtc	agctacaaca	cgggtgtcac	gctgttcggc	ggcttcgcgc	cgttcgtcat	1297
cacctggctg	atcagcgcga	cggcaaccg	gctgtcgccc	gcgctttatc	tgtatgggctg	1357
cgcggtgctg	agccttgccg	cgttggtcgt	cgcgcgcacg	cggctcaaga	tgcggtaacg	1417
caagaaacga	cggcgcagcg	atg	cgc	cgc	cgg	1470
		Met	Arg	Arg	Cys	Gly
		190	205	195	Pro	Pro
					Arg	Arg
					Arg	Arg
tgc	cgt	ggc	cgt	gct	gca	1518
Cys	Arg	Ala	Gly	Arg	Ala	
200	205	210	Pro	Phe	Thr	
act	gtc	cgc	tgt	gac	acc	1566
Thr	Val	Arg	Cys	Asp	Asp	
215	220	225	Asp	Thr	Asp	
gcg	att	agt	gca	acg	ggc	1620
Ala	Ile	Ser	Ala	Thr	Gly	
					Arg	
		235			Asn	
acttctgccc	agctcaccta	tccgcttac	ctgcag			1656

<210> SEQ ID NO 64

<211> LENGTH: 187

<212> TYPE: PRT

<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 64

Met	Val	Arg	Pro	Asp	Arg	Leu	Arg	Leu	Leu	Arg	Gly	Asp	Asp	Arg	Gln	
1						5			10					15		
Ala	Val	Leu	Pro	Arg	His	Glu	Arg	Ser	Asp	Ile	Ala	Asp	Ala	His	Ala	
						20			25					30		
Arg	His	Val	Arg	Ala	Val	Leu	Pro	Asp	Pro	Ala	Asp	Arg	Arg	Leu	Arg	
						35			40					45		
Ala	Arg	Arg	Ile	Arg	Arg	Ser	Ser	Gly	Pro	Gln	Gly	Val	Ala	Ala	Ala	
						50			55					60		
Val	Asp	Arg	Asp	Asp	Asp	Gly	Arg	His	Ala	Ala	Asp	Arg	Ala	Asp	Ala	
						65			70					75		80
Asp	Leu	Arg	Ile	Asp	Arg	His	Thr	Arg	Thr	Ala	Arg	Asp	His	Ala	Val	
						85			90					95		
Ala	Val	Asp	Ala	Gly	Leu	Phe	Arg	Gly	Arg	Ile	Arg	Glu	Leu	Asp		
						100			105					110		
Arg	Val	Pro	Arg	Arg	Ala	Arg	Ala	Ala	Ala	Ala	Arg	Phe	His	Val	Glu	
						115			120					125		
Leu	Ala	Val	Arg	Glu	Pro	Gly	Pro	Arg	Asp	Ala	Ala	Arg	Ile	Gly	Leu	
						130			135					140		
Arg	Cys	Ala	Ala	Asp	Ile	His	Ala	Asp	Ala	Cys	Ala	Thr	Arg	Lys	Leu	
						145			150					155		160
Gly	Leu	Ala	Arg	Ala	Val	Pro	Val	Arg	Ala	Arg	Asp	Arg	Pro	Gly	Arg	
						165			170					175		
Ala	Val	His	Pro	Pro	Leu	Arg	Arg	Arg	Arg							
						180			185							

<210> SEQ ID NO 65

<211> LENGTH: 51

<212> TYPE: PRT

<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 65

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Met Arg Arg Arg Cys Gly Pro Pro Arg Arg Arg Cys Arg Ala Gly Arg
 1 5 10 15
 Ala Pro Phe Thr Ala Pro Gly Ser Ala Ala Ala Thr Val Arg Cys Asp
 20 25 30
 Asp Thr Asp Ala Arg Lys Leu Thr Asn His Gly Ala Ile Ser Ala Thr
 35 40 45
 Gly Arg Asn
 50

<210> SEQ ID NO 66
<211> LENGTH: 2227
<212> TYPE: DNA
<213> ORGANISM: mosquito baculovirus
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (222)...(1253)
<400> SEQUENCE: 66

aagcttggcg ccgtgttcga gattctacga taccgcacga cctggaggta	aacttttagcgt	60
atccccaccag gttggatctg gacaagttgg ggctgggtt gagcttgcgc gcaattttacg		120
ttgcaaatcg gggtttaact ttcgagccgc gaaccgactc acccgagcgt gagtttcgtg		180
aaactagaag gcccactcgg cacaccaacg gtggtcccat a atg cgc ctc gaa gat	Met Arg Leu Glu Asp	236
1 5		
gaa ccg agc ctc gag gac cag atg att gat ttt ata aac aat aac cca		284
Glu Pro Ser Leu Glu Asp Gln Met Ile Asp Phe Ile Asn Asn Pro	10 15 20	
cta ata tcg agc ctg ctg gtt tca gcg ggt ttc gat ttc ata aac gac		332
Leu Ile Ser Ser Leu Leu Val Ser Ala Gly Phe Asp Phe Ile Asn Asp	25 30 35	
ggt ttc cgc gcc ctc atg aag aag gcc atg gtg cgg tac atc ccg atg		380
Gly Phe Arg Ala Leu Met Lys Lys Ala Met Val Arg Tyr Ile Pro Met	40 45 50	
ctg caa gcc gcc gca ata cgg ttc ggt gaa ggc ttg aca cgt aaa atg		428
Leu Gln Ala Ala Ile Arg Phe Gly Glu Gly Leu Thr Arg Lys Met	55 60 65	
gtc tcg gag gcg ttt cgt gtg ctc atg ttt agc cgc ata aac cag atg		476
Val Ser Glu Ala Phe Arg Val Leu Met Phe Ser Arg Ile Asn Gln Met	70 75 80 85	
gcc gtg cag ctg acc ggc gct cta gcg aag gca att gca cgc ttt ggt		524
Ala Val Gln Leu Thr Gly Ala Leu Ala Lys Ala Ile Ala Arg Phe Gly	90 95 100	
gcg atg gcc agt tcg gtg att gga atc gtg ttg ata ttt ttc gtc gca		572
Ala Met Ala Ser Ser Val Ile Gly Ile Val Leu Ile Phe Phe Val Ala	105 110 115	
gcc gat ata att ctc atg ttc tgg gac ccc tac ggt tac agc aac atg		620
Ala Asp Ile Ile Leu Met Phe Trp Asp Pro Tyr Gly Tyr Ser Asn Met	120 125 130	
ttt ccg ccc gag ttt ctg ggc gat ttg acg ctc aac ttt ctg tcg gcg		668
Phe Pro Pro Glu Phe Leu Gly Asp Leu Thr Leu Asn Phe Leu Ser Ala	135 140 145	
ttt ttc gag caa acg ggt acg cga aac gta atc gaa atg ata ccc caa		716
Phe Phe Glu Gln Thr Gly Thr Arg Asn Val Ile Glu Met Ile Pro Gln	150 155 160 165	
gcg tac gac tct atg gtg aaa ggt ggt gag gag gat gga ctc tac cta		764
Ala Tyr Asp Ser Met Val Lys Gly Gly Glu Glu Asp Gly Leu Tyr Leu	170 175 180	
aca ttt gcc gcc cta caa tac gtg agc cat atg gag gtg aac tcg gac		812

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Thr Phe Ala Ala Leu Gln Tyr Val Ser His Met Glu Val Asn Ser Asp			
185	190	195	
ggg cag ttg ttg ctg cta cga aac agt aac cca atc aag cag gag gaa		860	
Gly Gln Leu Leu Leu Leu Arg Asn Ser Asn Pro Ile Lys Gln Glu Glu			
200	205	210	
ctt gag ccg cac aac ctc acg gtg gcc ctc ttc ggc gct ata aac ctg		908	
Leu Glu Pro His Asn Leu Thr Val Ala Leu Phe Gly Ala Ile Asn Leu			
215	220	225	
cag agt tat gag gat ctt aag cgg cat atg gcc agc gcc aac cgg gcc		956	
Gln Ser Tyr Glu Asp Leu Lys Arg His Met Ala Ser Ala Asn Arg Ala			
230	235	240	245
ttc ggt ata gac ccc gaa acg ttg cag caa gtg gcc ccg tgg aga gat		1004	
Phe Gly Ile Asp Pro Glu Thr Leu Gln Gln Val Ala Pro Trp Arg Asp			
250	255	260	
aga ccc ggg aca gta att tca gct ggc gtc cta gtt gcg ctt gtg gtc		1052	
Arg Pro Gly Thr Val Ile Ser Ala Gly Val Leu Val Ala Leu Val Val			
265	270	275	
gtt ttg acc ggg agt caa ctt ttc agc aca aaa gcg ccc gat cta gct		1100	
Val Leu Thr Gly Ser Gln Leu Phe Ser Thr Lys Ala Pro Asp Leu Ala			
280	285	290	
acg gtg gtg ctc att gta att ctg gtg gcc ata gtg ata atc gtg cta		1148	
Thr Val Val Leu Ile Val Ile Leu Val Ala Ile Val Ile Ile Val Leu			
295	300	305	
caa ctc gac cgt ata aca ccc ctg gcc cga ctt gcc atc gta aag cat		1196	
Gln Leu Asp Arg Ile Thr Pro Leu Ala Arg Leu Ala Ile Val Lys His			
310	315	320	325
gaa gag aac gag aaa aat cgc gtc ggc caa cgc ttc gcc gga ctg ctt		1244	
Glu Glu Asn Glu Lys Asn Arg Val Gly Gln Arg Phe Ala Gly Leu Leu			
330	335	340	
aga cgt gct tgagcacccgc tacctaaccgg tggacctgcc cagctcgatg		1293	
Arg Arg Ala			
gaatttgcg cgaaaccgtt tgcgtatcac gtggggccg tacacggctt cgtggacgtg		1353	
agcaactgcg cgctggatgt gaccgtacgc gcacccagaa gctgtatccc ggaccgcata		1413	
gacctggagg ttaatttgcg cgtgtacaca aaggtggacg aatttttgc cgcaactgatc		1473	
cgacggccgg aaagtgggca caagtcggac gagctgtgca aacccgtatt gggctacttt		1533	
atggaagtgg tgtacggaaa ccggctaccg ttgacgaaat accagcgcga gaaaatgaaa		1593	
ctttttgtaa tgaacgcgt tcaccagcgc agggagcact tgggctacct gtatcggtta		1653	
cacctgaagg gtacggatgc gctgagaacc tttaccgagc acatgatgga aataaccgtc		1713	
gagcgcgaat tggaggacgg gtttccactg gggcccaatt tggtaaccct ttggacgcag		1773	
gactttcaga aggcgcctcaa cgctaagcga cacaatctacg gtgccgcggg cgaggaagac		1833	
acctgcggct gggatccgga aattttcatc gaactaaagc cccgcgcact gccagattt		1893	
cgcttcatga ccgtgtacaa gaaccacaag aagcggcatac cgctgttgt gctggaaacg		1953	
agcagtgc当地 cgaattcgc当地 aattttgc当地 aactattgc当地 aggagcgc当地 tttgagggt当地		2013	
tgggtcaaca gcaggaacaa ctgcctggtg gccgtggca cagatggagt caacttggat		2073	
tcatttgc当地 catttttaga tagttgtggt cgaccaatta ggccggcatt tcacacgaa		2133	
gtgtaccaat ttctcgaacg tggacggcca gatttgttct ttggcaacgc actgtttac		2193	
aacttttacc gatactctgg ccggtaacg gtga		2227	

<210> SEQ ID NO 67

<211> LENGTH: 344

<212> TYPE: PRT

<213> ORGANISM: mosquito baculovirus

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<400> SEQUENCE: 67

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Met Arg Leu Glu Asp Glu Pro Ser Leu Glu Asp Gln Met Ile Asp Phe
 1           5          10          15

Ile Asn Asn Asn Pro Leu Ile Ser Ser Leu Leu Val Ser Ala Gly Phe
 20          25          30

Asp Phe Ile Asn Asp Gly Phe Arg Ala Leu Met Lys Lys Ala Met Val
 35          40          45

Arg Tyr Ile Pro Met Leu Gln Ala Ala Ala Ile Arg Phe Gly Glu Gly
 50          55          60

Leu Thr Arg Lys Met Val Ser Glu Ala Phe Arg Val Leu Met Phe Ser
 65          70          75          80

Arg Ile Asn Gln Met Ala Val Gln Leu Thr Gly Ala Leu Ala Lys Ala
 85          90          95

Ile Ala Arg Phe Gly Ala Met Ala Ser Ser Val Ile Gly Ile Val Leu
100         105         110

Ile Phe Phe Val Ala Ala Asp Ile Ile Leu Met Phe Trp Asp Pro Tyr
115         120         125

Gly Tyr Ser Asn Met Phe Pro Pro Glu Phe Leu Gly Asp Leu Thr Leu
130         135         140

Asn Phe Leu Ser Ala Phe Phe Glu Gln Thr Gly Thr Arg Asn Val Ile
145         150         155         160

Glu Met Ile Pro Gln Ala Tyr Asp Ser Met Val Lys Gly Gly Glu Glu
165         170         175

Asp Gly Leu Tyr Leu Thr Phe Ala Ala Leu Gln Tyr Val Ser His Met
180         185         190

Glu Val Asn Ser Asp Gly Gln Leu Leu Leu Leu Arg Asn Ser Asn Pro
195         200         205

Ile Lys Gln Glu Glu Leu Glu Pro His Asn Leu Thr Val Ala Leu Phe
210         215         220

Gly Ala Ile Asn Leu Gln Ser Tyr Glu Asp Leu Lys Arg His Met Ala
225         230         235         240

Ser Ala Asn Arg Ala Phe Gly Ile Asp Pro Glu Thr Leu Gln Gln Val
245         250         255

Ala Pro Trp Arg Asp Arg Pro Gly Thr Val Ile Ser Ala Gly Val Leu
260         265         270

Val Ala Leu Val Val Val Leu Thr Gly Ser Gln Leu Phe Ser Thr Lys
275         280         285

Ala Pro Asp Leu Ala Thr Val Val Leu Ile Val Ile Leu Val Ala Ile
290         295         300

Val Ile Ile Val Leu Gln Leu Asp Arg Ile Thr Pro Leu Ala Arg Leu
305         310         315         320

Ala Ile Val Lys His Glu Glu Asn Glu Lys Asn Arg Val Gly Gln Arg
325         330         335

Phe Ala Gly Leu Leu Arg Arg Ala
340

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<210> SEQ ID NO 68

<211> LENGTH: 2227

<212> TYPE: DNA

<213> ORGANISM: mosquito baculovirus

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (1195)...(2223)

<400> SEQUENCE: 68

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aagcttggcg ccgttacga gattctacga taccgcacga cctggagggtg aactttacg	60
atcccaccag gttggatctg gacaagttgg ggctggggtt gagcttgcgc gcaatttacg	120
ttgcaaatacg gggtaact ttcgagccgc gaaccgactc acccgagcgt gagtttcgtg	180
aaactagaag gcccactcg cacaccaaac gtggtcccat aatgcgcctc gaagatgaac	240
c gagcctcga ggaccagatg attgatttta taaacaataa cccactaata tcgagcctgc	300
tggtttcagc gggtttcgt ttcataaaacg acggtttccg cgcctcatg aagaaggcca	360
tggtgccgta catccccatg ctgcaagccg cgcataacg gttcgggtaa ggcttgacac	420
gtaaaatggt ctcggaggcg tttcgtgtc tcatgttttag cgcataaac cagatggccg	480
tgcagctgac cggcgtctca gcgaaggcaa ttgcacgctt tggtgcgtatg gccagttcgg	540
tgatttgaat cgttgtgata ttttcgtcg cagccgatata aattctcatg ttctgggacc	600
cgtacggta cagcaacatg tttccggcccg agtttctggg cgatttgacg ctcaacttgc	660
tgcggcggtt ttcgagcaa acgggtacgc gaaacgtaat cgaatgtata ccccaaggcgt	720
acgactctat ggtgaaagggt ggtgaggagg atggactcta cctaacattt gcccgcctac	780
aatacgtgag ccataatggg gtgaaactcggtt acgggcgtt tggctgtcta cggaaacagta	840
acccaaatcaa gcaggaggaa cttgagccgc acaacctcac ggtggccctc ttccgcgtca	900
taaacatcgca gagttatgag gatcttaagc ggcataatggc cagcgcac cggccgtcg	960
gtatagaccc cggaaacgttg cagcaagtgg ccccggtggag agatagaccc gggacagtaa	1020
tttcagctgg cgtcttagtt gcgttgcgtt tggctgtgttgc cggagtcata cttttcagca	1080
caaaagcgcc cggatctatgtt acgggtgtgc tcattgtata tctgggtggcc atagtataa	1140
tcgtgttaca actcgaccgt ataacaccccc tggcccgact tgccatcgta aagc atg Met 1	1197
aag aga acg aga aaa atc gcg tcg gcc aac gct tcg ccg gac tgc tta Lys Arg Thr Arg Lys Ile Ala Ser Ala Asn Ala Ser Pro Asp Cys Leu 5 10 15	1245
gac gtg ctt gag cac cgc tac cta acg gtg gac ctg ccc agc tcg atg Asp Val Leu Glu His Arg Tyr Leu Thr Val Asp Leu Pro Ser Ser Met 20 25 30	1293
gaa ttt tgc gcg aaa ccg ttt gcg tat cac gtg gtg gcc gta cac ggc Glu Phe Cys Ala Lys Pro Phe Ala Tyr His Val Val Ala Val His Gly 35 40 45	1341
ttc gtg gac gtg agc aac tgc gcg ctg gat gtg acc gta cgc gca ccc Phe Val Asp Val Ser Asn Cys Ala Leu Asp Val Thr Val Arg Ala Pro 50 55 60 65	1389
aga agc tgt atc ccg gac cgc ata gac ctg gag gtt aat ttg cgc gtg Arg Ser Cys Ile Pro Asp Arg Ile Asp Leu Glu Val Asn Leu Arg Val 70 75 80	1437
tac aca aag gtg gac gaa ttt ttt gcc gca ctg atc cga ccg ccg gaa Tyr Thr Lys Val Asp Glu Phe Phe Ala Ala Leu Ile Arg Arg Pro Glu 85 90 95	1485
agt ggg cac aag tcg gac gag ctg tgc aaa ccc gta ttg ggc tac ttt Ser Gly His Lys Ser Asp Glu Leu Cys Lys Pro Val Leu Gly Tyr Phe 100 105 110	1533
atg gaa gtg gtg tac gga aac cgg cta ccg ttg acg aaa tac cag cgc Met Glu Val Val Tyr Gly Asn Arg Leu Pro Leu Thr Lys Tyr Gln Arg 115 120 125	1581
gag aaa atg aaa ctt ttt gta atg aac gcg att cac cag cgc agg gag Glu Lys Met Lys Leu Phe Val Met Asn Ala Ile His Gln Arg Arg Glu 130 135 140 145	1629

-continued

cac ttg ggc tac ctg tat cgg gta cac ctg aag ggt acg gat gcg ctg His Leu Gly Tyr Leu Tyr Arg Val His Leu Lys Gly Thr Asp Ala Leu 150 155 160	1677
aga acc ttt acc gag cac atg atg gaa ata acc gtc gag cgc aag ttg Arg Thr Phe Thr Glu His Met Met Glu Ile Thr Val Glu Arg Lys Leu 165 170 175	1725
gag gac ggg ttt cca ctg ggg ccc aat ttg gta acc ctt tgg acg cag Glu Asp Gly Phe Pro Leu Gly Pro Asn Leu Val Thr Leu Trp Thr Gln 180 185 190	1773
gac ttt cag aag gcg ctc aac gct aag cga cac atc tac ggt gcc gcg Asp Phe Gln Lys Ala Leu Asn Ala Lys Arg His Ile Tyr Gly Ala Ala 195 200 205	1821
ggc gag gaa gac acc tgc ggc tgg gat ccg gaa att ttc atc gaa cta Gly Glu Glu Asp Thr Cys Gly Trp Asp Pro Glu Ile Phe Ile Glu Leu 210 215 220 225	1869
aag ccc gcc gca ctg cca gat tta cgc ttc atg acc gtg tac aag aac Lys Pro Ala Ala Leu Pro Asp Leu Arg Phe Met Thr Val Tyr Lys Asn 230 235 240	1917
cac aag aag cgg cat ccg ctg ctg gtg ctg gaa acg agc agt gca acg His Lys Arg His Pro Leu Leu Val Leu Glu Thr Ser Ser Ala Thr 245 250 255	1965
aat tcg caa att ttt gca aac tat tgc gag gag cgc ggt ttg agg tgt Asn Ser Gln Ile Phe Ala Asn Tyr Cys Glu Glu Arg Gly Leu Arg Cys 260 265 270	2013
tgg gtc aac agc agg aac aac tgc ctg gtg gcc gtg ggc aca gat gga Trp Val Asn Ser Arg Asn Asn Cys Leu Val Ala Val Gly Thr Asp Gly 275 280 285	2061
gtc aac ttg gat tca ttg gcc gca ttt tta gat agt tgt ggt cga cca Val Asn Leu Asp Ser Leu Ala Ala Phe Leu Asp Ser Cys Gly Arg Pro 290 295 300 305	2109
att agg ccg gca ttt cac acg aac gtg tac caa ttt ctc gaa cgt gga Ile Arg Pro Ala Phe His Thr Asn Val Tyr Gln Phe Leu Glu Arg Gly 310 315 320	2157
cgg cca gat ttg ttc ttt ggc aac gca ctg ttt tac aac ttt tac cga Arg Pro Asp Leu Phe Phe Gly Asn Ala Leu Phe Tyr Asn Phe Tyr Arg 325 330 335	2205
tac tct ggc cgg tta acg gtga Tyr Ser Gly Arg Leu Thr 340	2227

<210> SEQ ID NO 69
<211> LENGTH: 343
<212> TYPE: PRT
<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 69

Met Lys Arg Thr Arg Lys Ile Ala Ser Ala Asn Ala Ser Pro Asp Cys 1 5 10 15
Leu Asp Val Leu Glu His Arg Tyr Leu Thr Val Asp Leu Pro Ser Ser 20 25 30
Met Glu Phe Cys Ala Lys Pro Phe Ala Tyr His Val Val Ala Val His 35 40 45
Gly Phe Val Asp Val Ser Asn Cys Ala Leu Asp Val Thr Val Arg Ala 50 55 60
Pro Arg Ser Cys Ile Pro Asp Arg Ile Asp Leu Glu Val Asn Leu Arg 65 70 75 80
Val Tyr Thr Lys Val Asp Glu Phe Phe Ala Ala Leu Ile Arg Arg Pro 85 90 95
Glu Ser Gly His Lys Ser Asp Glu Leu Cys Lys Pro Val Leu Gly Tyr

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100	105	110
Phe Met Glu Val Val Tyr Gly Asn Arg Leu Pro Leu Thr Lys Tyr Gln		
115	120	125
Arg Glu Lys Met Lys Leu Phe Val Met Asn Ala Ile His Gln Arg Arg		
130	135	140
Glu His Leu Gly Tyr Leu Tyr Arg Val His Leu Lys Gly Thr Asp Ala		
145	150	155
Leu Arg Thr Phe Thr Glu His Met Met Glu Ile Thr Val Glu Arg Lys		
165	170	175
Leu Glu Asp Gly Phe Pro Leu Gly Pro Asn Leu Val Thr Leu Trp Thr		
180	185	190
Gln Asp Phe Gln Lys Ala Leu Asn Ala Lys Arg His Ile Tyr Gly Ala		
195	200	205
Ala Gly Glu Glu Asp Thr Cys Gly Trp Asp Pro Glu Ile Phe Ile Glu		
210	215	220
Leu Lys Pro Ala Ala Leu Pro Asp Leu Arg Phe Met Thr Val Tyr Lys		
225	230	235
Asn His Lys Lys Arg His Pro Leu Leu Val Leu Glu Thr Ser Ser Ala		
245	250	255
Thr Asn Ser Gln Ile Phe Ala Asn Tyr Cys Glu Glu Arg Gly Leu Arg		
260	265	270
Cys Trp Val Asn Ser Arg Asn Asn Cys Leu Val Ala Val Gly Thr Asp		
275	280	285
Gly Val Asn Leu Asp Ser Leu Ala Ala Phe Leu Asp Ser Cys Gly Arg		
290	295	300
Pro Ile Arg Pro Ala Phe His Thr Asn Val Tyr Gln Phe Leu Glu Arg		
305	310	315
Gly Arg Pro Asp Leu Phe Phe Gly Asn Ala Leu Phe Tyr Asn Phe Tyr		
325	330	335
Arg Tyr Ser Gly Arg Leu Thr		
340		

<210> SEQ ID NO 70
<211> LENGTH: 2227
<212> TYPE: DNA
<213> ORGANISM: mosquito baculovirus
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1639)...(2109)

<400> SEQUENCE: 70

tcaccgttaa ccggccagag tatkgtaaaa agttgtaaaa cagtgcgttg ccaaagaaca	60
aatctggccg tccacgttgc agaaatttgtt acacgttgcgt gtgaaatgcc ggcctaattt	120
gtcgaccaca actatctaaa aatcgccca atgaatccaa ttgtactcca tctgtgccc	180
cggccaccag gcagttgttc ctgtgttgc cccaaacacct caaacccgcgc tcctcgcaat	240
agtttgcaaa aatttgcgaa ttctgtgcac tgctcggttgc cagcaccaggc agcggatgcc	300
gtttcttgcgtt gttcttgcgt acggcatgc acgttaatc tggcagtgcgc gccccgttta	360
gttcgtatgaa aatttccgaa tcccaacttgc aggtgtcttc ctgcgttgcgc gcaccgttgc	420
tgtgtcgctt agcgttgagc gccttctgaa agtccgtgcgtt ccaaagggtt accaaattgg	480
gccccagttgg aaaccctgtcc tccaaacttgc gctcgacgtt tatttccatc atgtgtcg	540
taaagggttct cagcgtatcc gtacccttca ggtgtacccg atacaggtag cccaaatgtct	600
ccctgtcgctt gtgaatcgcc ttcattacaa aaagtttcat tttctcgccgc tggtatccg	660

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tcaacggtag ccgggttccg tacaccactt ccataaaatgc gccaatacg ggtttgac	720
gctcgtccga cttgtgccc cttccggcc gtccggatcg tgccggaaaa aattcgcca	780
cctttgtta cacgcgcaaa ttaacctcca ggtctatgcg gtccggata cagttctgg	840
gtgcgcgtac ggtcacatcc agcgcgcagt tgctcacgtc cacgaagccg tgtacggca	900
ccacgtgata cgcaaacggt ttccgcgaaa attccatcga gctggcagg tccaccgtta	960
ggtagccgtg ctcaagcagc tctaaggcgt ccggcgaagc gttggccgac gcgattttc	1020
tcgttctctt catgtttaac gatggcaagt cggccagggt gtgttatacg gtcgagttgt	1080
agcacgatta tcactatggc caccagaatt acaatgagca ccaccgtac tagatcgccc	1140
gcttttgtc tgaaaagttg actcccggtc aaaacgacca caagcgcaac taggacgcca	1200
gctgaaattt ctgtccccgg tctatctctc cacggggcca cttgctgcaaa cgtttcgggg	1260
tctataccga aggcccggtt ggcgctggcc atatgccgt taagatcctc ataactctgc	1320
aggtttatacg cgccgaagag ggccaccgtg aggttgcgtc gctcaagttc ctccctgttt	1380
attgggttac tgtttcgttag cagcaacaac tgcccggtcg agttcacctc catatggctc	1440
acgtattgtt gggccggaaa tggtaggttag agtccatctt cctcaccacc tttcaccata	1500
gagtcgtacg cttgggttat catttcgatt acgtttcggt taccgggttgc tctgaaaaac	1560
gccgacagaa agttgagcgt ccaaatacgccc agaaaactcggt gcggaaacat gttgctgtaa	1620
ccgtacgggt cccagaac atg aga att ata tcg gct gcg acg aaa aat atc Met Arg Ile Ile Ser Ala Ala Thr Lys Asn Ile	1671
1 5 10	
aac acg att cca atc acc gaa ctg gcc atc gca cca aag cgt gca att Asn Thr Ile Pro Ile Thr Glu Leu Ala Ile Ala Pro Lys Arg Ala Ile	1719
15 20 25	
gcc ttc gct aga gcg ccg gtc agc tgc acg gcc atc tgg ttt atg cgg Ala Phe Ala Arg Ala Pro Val Ser Cys Thr Ala Ile Trp Phe Met Arg	1767
30 35 40	
cta aac atg agc aca cga aac gcc tcc gag acc att tta cgt gtc aag Leu Asn Met Ser Thr Arg Asn Ala Ser Glu Thr Ile Leu Arg Val Lys	1815
45 50 55	
cct tca ccg aac cgt att gcg gcg gct tgc agc atc ggg atg tac cgc Pro Ser Pro Asn Arg Ile Ala Ala Cys Ser Ile Gly Met Tyr Arg	1863
60 65 70 75	
acc atg gcc ttc atg agg gcg ccg aaa ccg tcg ttt atg aaa tcg Thr Met Ala Phe Met Arg Ala Arg Lys Pro Ser Phe Met Lys Ser	1911
80 85 90	
aaa ccc gct gaa acc agc agg ctc gat att agt ggg tta ttg ttt ata Lys Pro Ala Glu Thr Ser Arg Leu Asp Ile Ser Gly Leu Leu Phe Ile	1959
95 100 105	
aaa tca atc atc tgg tcc tcg agg ctc ggt tca tct tcg agg cgc att Lys Ser Ile Ile Trp Ser Ser Arg Leu Gly Ser Ser Arg Arg Ile	2007
110 115 120	
atg gga cca ccg ttg gtg tgc cga gtg ggc ctt cta gtt tca cga aac Met Gly Pro Pro Leu Val Cys Arg Val Gly Leu Leu Val Ser Arg Asn	2055
125 130 135	
tca cgc tcg ggt gag tcg gtt cgc ggc tcg aaa gtt aaa ccc cga ttt Ser Arg Ser Gly Glu Ser Val Arg Gly Ser Lys Val Lys Pro Arg Phe	2103
140 145 150 155	
gca acg taaattgcgc gcaagctaa ccccaagcccc aacttgtcca gatccaacct Ala Thr	2159
ggtggatcg ctaaaatgtca cttccagggtc gtgcggatc gttagaatctc gaacacggcg	2219
ccaagctt	2227

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<210> SEQ ID NO 71
<211> LENGTH: 157
<212> TYPE: PRT
<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 71

Met Arg Ile Ile Ser Ala Ala Thr Lys Asn Ile Asn Thr Ile Pro Ile
 1           5           10          15

Thr Glu Leu Ala Ile Ala Pro Lys Arg Ala Ile Ala Phe Ala Arg Ala
20           25           30

Pro Val Ser Cys Thr Ala Ile Trp Phe Met Arg Leu Asn Met Ser Thr
35           40           45

Arg Asn Ala Ser Glu Thr Ile Leu Arg Val Lys Pro Ser Pro Asn Arg
50           55           60

Ile Ala Ala Ala Cys Ser Ile Gly Met Tyr Arg Thr Met Ala Phe Phe
65           70           75           80

Met Arg Ala Arg Lys Pro Ser Phe Met Lys Ser Lys Pro Ala Glu Thr
85           90           95

Ser Arg Leu Asp Ile Ser Gly Leu Leu Phe Ile Lys Ser Ile Ile Trp
100          105          110

Ser Ser Arg Leu Gly Ser Ser Arg Arg Ile Met Gly Pro Pro Leu
115          120          125

Val Cys Arg Val Gly Leu Leu Val Ser Arg Asn Ser Arg Ser Gly Glu
130          135          140

Ser Val Arg Gly Ser Lys Val Lys Pro Arg Phe Ala Thr
145          150          155

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<210> SEQ ID NO 72
<211> LENGTH: 827
<212> TYPE: DNA
<213> ORGANISM: mosquito baculovirus
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (256)....(693)

<400> SEQUENCE: 72

aagcttgacg gtgttcgggg caaggcgatc gttgagcccc acgagggcca ccaccggatc      60
caccttgcgc tggacgatga gcgtggattt ttgttctcgat taccggcggt cttgcacgac      120
cgggcgtggg tttcacgggc ggggctaactg ctgctgcagg tcgagttacgt ggaacagatt      180
gaaacctttt tcgtcgtggc cgtgctttgtt gtgcacggct ttggcttacact gtacggcgcc      240
tgttacgttg acgag atg caa aat tac cgc agc tta acg ttg gac tcg atc      291
    Met Gln Asn Tyr Arg Ser Leu Thr Leu Asp Ser Ile
    1           5           10

acc atg ctt cgt tcg ggc aac ctg gcc gac aag ttg acc ctg tac gac      339
Thr Met Leu Arg Ser Gly Asn Ala Asp Lys Leu Thr Leu Tyr Asp
    15          20          25

cac att gac cac tcg cca aca atg tac agc ttg gcg aca caa ttt ttc      387
His Ile Asp His Ser Pro Thr Met Tyr Ser Leu Ala Thr Gln Phe Phe
    30          35          40

gtc cgc ggt aaa cgg gcc aac agt acg ctc gcg gac ccc atg ggt gaa      435
Val Arg Gly Lys Arg Ala Asn Ser Thr Leu Ala Asp Pro Met Gly Glu
    45          50          55          60

cag ttt tgg cac gcg cac gga gca cca ctg gac ggc cgt atc gtg gta      483
Gln Phe Trp His Ala His Gly Ala Pro Leu Asp Gly Arg Ile Val Val
    65          70          75

act aga agt ggg gac cta tac aag tta aag tgt gaa aaa tcg tac gaa      531

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Thr Arg Ser Gly Asp Leu Tyr Lys Leu Lys Cys Glu Lys Ser Tyr Glu			
80	85	90	
ctt cga ttc aac gga gcc caa ctc gag gat gcg gtc ggg aaa acg ttc		579	
Leu Arg Phe Asn Gly Ala Gln Leu Glu Asp Ala Val Gly Lys Thr Phe			
95	100	105	
att ccg agt cgg gtt gac ctc gag ccc gac acc atc tac gag tgt act		627	
Ile Pro Ser Arg Val Asp Leu Glu Pro Asp Thr Ile Tyr Glu Cys Thr			
110	115	120	
atc gtg gac aat ttt gcc acg gtt aag cgg gcc agg ttg gac agg gct		675	
Ile Val Asp Asn Phe Ala Thr Val Lys Arg Ala Arg Leu Asp Arg Ala			
125	130	135	140
acg gcg aat acg gtt gaa taaagagtaa attgttatta ttaatacact		723	
Thr Ala Asn Thr Val Glu			
145			
tgttgttgg tttcattcaa atagaaggaa aagaataaa gtttatcctc agtgaggctc		783	
gaggttgtcc gactgggtgg tggtcgtcag gggcgaataa gctt		827	

<210> SEQ ID NO 73
<211> LENGTH: 146
<212> TYPE: PRT
<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 73

Met Gln Asn Tyr Arg Ser Leu Thr Leu Asp Ser Ile Thr Met Leu Arg			
1	5	10	15
Ser Gly Asn Leu Ala Asp Lys Leu Thr Leu Tyr Asp His Ile Asp His			
20	25	30	
Ser Pro Thr Met Tyr Ser Leu Ala Thr Gln Phe Phe Val Arg Gly Lys			
35	40	45	
Arg Ala Asn Ser Thr Leu Ala Asp Pro Met Gly Glu Gln Phe Trp His			
50	55	60	
Ala His Gly Ala Pro Leu Asp Gly Arg Ile Val Val Thr Arg Ser Gly			
65	70	75	80
Asp Leu Tyr Lys Leu Lys Cys Glu Lys Ser Tyr Glu Leu Arg Phe Asn			
85	90	95	
Gly Ala Gln Leu Glu Asp Ala Val Gly Lys Thr Phe Ile Pro Ser Arg			
100	105	110	
Val Asp Leu Glu Pro Asp Thr Ile Tyr Glu Cys Thr Ile Val Asp Asn			
115	120	125	
Phe Ala Thr Val Lys Arg Ala Arg Leu Asp Arg Ala Thr Ala Asn Thr			
130	135	140	
Val Glu			
145			

<210> SEQ ID NO 74
<211> LENGTH: 827
<212> TYPE: DNA
<213> ORGANISM: mosquito baculovirus
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (214)...(561)

<400> SEQUENCE: 74

aagcttattc gcccctgacg accaccaccc agtcggacaa cctcgagcct cactgaggat		60
aaactttatt tccttccctt ctatttgaat gaaaaccaac aacaagtgtt ttaataataa		120
caatttactc tttattcaac cgtattcgcc gtagccctgt ccaacctggc cccgcttaacc		180
gtggcaaaat tgtccacgat agtacactcg tag atg gtg tcg ggc tcg agg tca		234

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Met Val Ser Gly Ser Arg Ser		
1	5	
acc cga ctc gga atg aac gtt ttc ccg acc gca tcc tcg agt tgg gct		282
Thr Arg Leu Gly Met Asn Val Phe Pro Thr Ala Ser Ser Ser Trp Ala		
10 15 20		
ccg ttg aat cga agt tcg tac gat ttt tca cac ttt aac ttg tat agg		330
Pro Leu Asn Arg Ser Ser Tyr Asp Phe Ser His Phe Asn Leu Tyr Arg		
25 30 35		
tcc cca ctt cta gtt acc acg ata cgg ccg tcc agt ggt gct ccg tgc		378
Ser Pro Leu Leu Val Thr Thr Ile Arg Pro Ser Ser Gly Ala Pro Cys		
40 45 50 55		
gcg tgc caa aac tgt tca ccc atg ggg tcc gcg agc gta ctg ttg gcc		426
Ala Cys Gln Asn Cys Ser Pro Met Gly Ser Ala Ser Val Leu Leu Ala		
60 65 70		
cgt tta ccg cgg acg aaa aat tgt gtc gcc aag ctg tac att gtt ggc		474
Arg Leu Pro Arg Thr Lys Asn Cys Val Ala Lys Leu Tyr Ile Val Gly		
75 80 85		
gag tgg tca atg tgg tcg tac agg gtc aac ttg tcg gcc agg ttg ccc		522
Glu Trp Ser Met Trp Ser Tyr Arg Val Asn Leu Ser Ala Arg Leu Pro		
90 95 100		
gaa cga agc atg gtg atc gag tcc aac gtt aag ctg cgg taatttgca		571
Glu Arg Ser Met Val Ile Glu Ser Asn Val Lys Leu Arg		
105 110 115		
tctcgtaac gtaacagccg ccgtacaggt agccaaagcc gtgcacacca agcacgtcca		631
cgacgaaaaa ggttcaatc tgttccacgt actcgacctg cagcagcggt agccccgccc		691
gtgaaaccca cggccggctg tgcaagccgc cgggttaacga gaacaaaaat ccacgctcat		751
cgtccagcgc aagggtggatc cggtggtggc cctcgtgggg ctcaacgatc gccttgcggc		811
gaacaccgtc aagctt		827

<210> SEQ ID NO 75

<211> LENGTH: 116

<212> TYPE: PRT

<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 75

Met Val Ser Gly Ser Arg Ser Thr Arg Leu Gly Met Asn Val Phe Pro		
1	5	10 15
Thr Ala Ser Ser Ser Trp Ala Pro Leu Asn Arg Ser Ser Tyr Asp Phe		
20 25 30		
Ser His Phe Asn Leu Tyr Arg Ser Pro Leu Leu Val Thr Thr Ile Arg		
35 40 45		
Pro Ser Ser Gly Ala Pro Cys Ala Cys Gln Asn Cys Ser Pro Met Gly		
50 55 60		
Ser Ala Ser Val Leu Leu Ala Arg Leu Pro Arg Thr Lys Asn Cys Val		
65 70 75 80		
Ala Lys Leu Tyr Ile Val Gly Glu Trp Ser Met Trp Ser Tyr Arg Val		
85 90 95		
Asn Leu Ser Ala Arg Leu Pro Glu Arg Ser Met Val Ile Glu Ser Asn		
100 105 110		
Val Lys Leu Arg		
115		

<210> SEQ ID NO 76

<211> LENGTH: 692

<212> TYPE: DNA

<213> ORGANISM: mosquito baculovirus

<220> FEATURE:

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<221> NAME/KEY: CDS
<222> LOCATION: (27)...(689)

<400> SEQUENCE: 76

gaattcaatg tcatgtggcc cgaccg atg tcc cag ctc ctg ctc aac ccc aag	53
Met Ser Gln Leu Leu Asn Pro Lys	
1 5	
ccc ctg gta tcg gaa ctg gaa gcc ccg atg gtt ggt caa ctt gtg ggt	101
Pro Leu Val Ser Glu Leu Glu Ala Pro Met Val Gly Gln Leu Val Gly	
10 15 20 25	
aat acg gaa atc gag caa aaa atc gta cga act gtt gcc agc gaa tat	149
Asn Thr Glu Ile Glu Gln Lys Ile Val Arg Thr Val Ala Ser Glu Tyr	
30 35 40	
gca gct cat cga cat cta att cgg cgc tgc atg ccg ttt cgg cag	197
Ala Ala His Arg His Leu Ile Arg Arg Cys Leu Met Pro Phe Arg Gln	
45 50 55	
aac gtt ctg cag ggt tgc tac aac gaa gtc gta cgg tac gtc gag	245
Asn Val Leu Gln Gly Cys Tyr Asn Glu Val Val Arg Tyr Val Val Glu	
60 65 70	
att caa acc agc cgc ata cta ttt tac cag cac gac ttg gaa cat tat	293
Ile Gln Thr Ser Arg Ile Leu Phe Tyr Gln His Asp Leu Glu His Tyr	
75 80 85	
tgt gtg gtc agc aag ccg ccc cac ttg gcc tca cac tac ggc gac tgc	341
Cys Val Val Ser Lys Pro Pro His Leu Ala Ser His Tyr Gly Asp Cys	
90 95 100 105	
tat tgc gag gtc aac ctg agc tcc aca ccg atg gtg aca ctg gat gtg	389
Tyr Cys Glu Val Asn Leu Ser Ser Thr Pro Met Val Thr Leu Asp Val	
110 115 120	
gcg cga gag ttt gtg agc ccg ctg ttg gat gaa att tgc aaa cag	437
Ala Arg Glu Phe Val Ser Pro Leu Leu Asp Glu Ile Cys Lys Gln	
125 130 135	
gtt aac ttt ccg gtg cac agc gag ccc cag ttg tcc gca tat ctg tac	485
Val Asn Phe Pro Val His Ser Glu Pro Gln Leu Ser Ala Tyr Leu Tyr	
140 145 150	
aca ata cga att gca ggt aag ttt gta cgt gtg act cac gtt cgc aac	533
Thr Ile Arg Ile Ala Gly Lys Phe Val Arg Val Thr His Val Arg Asn	
155 160 165	
gag tat tgg tac tgc gtg gcg gac ctg aag ctg gcg gtc gac gga aca	581
Glu Tyr Trp Tyr Cys Val Ala Asp Leu Lys Leu Ala Val Asp Gly Thr	
170 175 180 185	
aaa acg cgc aaa ctg ttc gaa ctc caa ccc ggg cac gat ttg cgc cct	629
Lys Thr Arg Lys Leu Phe Glu Leu Gln Pro Gly His Asp Leu Arg Pro	
190 195 200	
gac gaa tac ccc ttg ctg ttt gtg aat cag cga cac ctg cgg ccc gcc	677
Asp Glu Tyr Pro Leu Leu Phe Val Asn Gln Arg His Leu Arg Pro Ala	
205 210 215	
aac gac cac gaa ttc	692
Asn Asp His Glu	
220	

<210> SEQ ID NO 77
<211> LENGTH: 221
<212> TYPE: PRT
<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 77

Met Ser Gln Leu Leu Asn Pro Lys Pro Leu Val Ser Glu Leu Glu	
1 5 10 15	
Ala Pro Met Val Gly Gln Leu Val Gly Asn Thr Glu Ile Glu Gln Lys	
20 25 30	

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ccaacgacca cgaattc	692
<210> SEQ ID NO 79	
<211> LENGTH: 51	
<212> TYPE: PRT	
<213> ORGANISM: mosquito baculovirus	
<400> SEQUENCE: 79	
Met Lys Pro Asp Arg Cys Pro Ser Ser Cys Ser Thr Pro Ser Pro Trp	
1 5 10 15	
Tyr Arg Asn Trp Lys Pro Arg Trp Leu Val Asn Leu Trp Val Ile Arg	
20 25 30	
Lys Ser Ser Lys Lys Ser Tyr Glu Leu Leu Pro Ala Asn Met Gln Leu	
35 40 45	
Ile Asp Ile	
50	
<210> SEQ ID NO 80	
<211> LENGTH: 692	
<212> TYPE: DNA	
<213> ORGANISM: mosquito baculovirus	
<220> FEATURE:	
<221> NAME/KEY: CDS	
<222> LOCATION: (1)...(366)	
<221> NAME/KEY: CDS	
<222> LOCATION: (529)...(690)	
<400> SEQUENCE: 80	
gaa ttc gtg gtc gtt ggc ggg ccg cag gtg tcg ctg att cac aaa cag	48
Glu Phe Val Val Val Gly Gly Pro Gln Val Ser Leu Ile His Lys Gln	
1 5 10 15	
caa ggg gta ttc gtc agg gcg caa atc gtg ccc ggg ttg gag ttc gaa	96
Gln Gly Val Phe Val Arg Ala Gln Ile Val Pro Gly Leu Glu Phe Glu	
20 25 30	
cag ttt gcg cgt ttt tgt tcc gtc gac cgc cag ctt cag gtc cgc cac	144
Gln Phe Ala Arg Phe Cys Ser Val Asp Arg Gln Leu Gln Val Arg His	
35 40 45	
gca gta cca ata ctc gtt gcg aac gtg agt cac acg tac aaa ctt acc	192
Ala Val Pro Ile Leu Val Ala Asn Val Ser His Thr Tyr Lys Leu Thr	
50 55 60	
tgc aat tcg tat tgt gta cag ata tgc gga caa ctg ggg ctc gct gtg	240
Cys Asn Ser Tyr Cys Val Gln Ile Cys Gly Gln Leu Gly Leu Ala Val	
65 70 75 80	
cac cgg aaa gtt aac ctg ttt gca aat ttc atc caa cag cag cgg gct	288
His Arg Lys Val Asn Leu Phe Ala Asn Phe Ile Gln Gln Gln Arg Ala	
85 90 95	
cac aaa ctc tcg cgc cac atc cag tgt cac cat cgg tgt gga gct cag	336
His Lys Leu Ser Arg His Ile Gln Cys His Arg Cys Gly Ala Gln	
100 105 110	
gtt gac ctc gca ata gca gtc gcc gta gtg tgaggccaag tggggcggt	386
Val Asp Leu Ala Ile Ala Val Ala Val Val	
115 120	
tgctgaccac acaataatgt tccaaagtctgt gctggtaaaa tagtatgcgg ctgggtttgaa	446
tctcgacgac gtaccgtacg acttcgttgtt acgaaccctg cagaacgttc tgccgaaacg	506
gcatcaggca gcgccgaatt ag atg tcg atg agc tgc ata ttc gct ggc aac	558
Met Ser Met Ser Cys Ile Phe Ala Gly Asn	
125 130	
agt tcg tac gat ttt ttg ctc gat ttc cgt att acc cac aag ttg acc	606
Ser Ser Tyr Asp Phe Leu Leu Asp Phe Arg Ile Thr His Lys Leu Thr	
135 140 145	

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aac cat cgg ggc ttc cag ttc cga tac cag ggg ctt ggg gtt gag cag Asn His Arg Gly Phe Gln Phe Arg Tyr Gln Gly Leu Gly Val Glu Gln 150 155 160	654
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gag ctg gga cat cgg tcg ggc ttc atc aca ttg aat tc Glu Leu Gly His Arg Ser Gly Phe Ile Thr Leu Asn 165 170 175	692
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<210> SEQ ID NO 81
<211> LENGTH: 122
<212> TYPE: PRT
<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 81

Glu Phe Val Val Val Gly Gly Pro Gln Val Ser Leu Ile His Lys Gln 1 5 10 15
--

Gln Gly Val Phe Val Arg Ala Gln Ile Val Pro Gly Leu Glu Phe Glu 20 25 30

Gln Phe Ala Arg Phe Cys Ser Val Asp Arg Gln Leu Gln Val Arg His 35 40 45

Ala Val Pro Ile Leu Val Ala Asn Val Ser His Thr Tyr Lys Leu Thr 50 55 60

Cys Asn Ser Tyr Cys Val Gln Ile Cys Gly Gln Leu Gly Leu Ala Val 65 70 75 80
--

His Arg Lys Val Asn Leu Phe Ala Asn Phe Ile Gln Gln Gln Arg Ala 85 90 95

His Lys Leu Ser Arg His Ile Gln Cys His His Arg Cys Gly Ala Gln 100 105 110
--

Val Asp Leu Ala Ile Ala Val Ala Val Val 115 120
--

<210> SEQ ID NO 82
<211> LENGTH: 54
<212> TYPE: PRT
<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 82

Met Ser Met Ser Cys Ile Phe Ala Gly Asn Ser Ser Tyr Asp Phe Leu 1 5 10 15
--

Leu Asp Phe Arg Ile Thr His Lys Leu Thr Asn His Arg Gly Phe Gln 20 25 30

Phe Arg Tyr Gln Gly Leu Gly Val Glu Gln Glu Leu Gly His Arg Ser 35 40 45

Gly Phe Ile Thr Leu Asn 50

<210> SEQ ID NO 83
<211> LENGTH: 3198
<212> TYPE: DNA
<213> ORGANISM: mosquito baculovirus
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (2545)...(3198)
<221> NAME/KEY: CDS
<222> LOCATION: (742)...(1056)
<221> NAME/KEY: CDS
<222> LOCATION: (1837)...(1998)

<400> SEQUENCE: 83

gaattcgcaa tcaagctgcc actttgccc ctgttagctaa ttgtgcggga taacgagtcc 60

acgctaaagt cctcccttgc aatttacgc aaatcttcaa gaaaaatac cgtagctaaa 120
--

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ctgtacgaaa gggccccc ttcgcacaac ttcatcgat actcgatcca tcgctttag	180
caccggacga tggctctggt caaattctg cccacaaaaa gtcccccata cttgtagata	240
ttgtcggcaa tgtaaacac gtacgacttt ttgcgggtgtg taaacacgga cgaccgcaca	300
atcaactcga gcgcatttata ataaccgacg cccacagttt tcgccaatcc agcggaaaaa	360
tgttcaatta aaccggaaa cgcattcggg tccaccgtta caccgctggt gggctgcata	420
aatttaaaca tgatcaatc ggtgtctccg taaacgaaaa atgcgcacag gccgtactgc	480
tcattccagt actcggtgt gtaattgacc gctgatcgaa ctttaccgcg gccagtttt	540
gtgataaaagt ttccaaacgg tggaaaccgt agcgaaaga aaccgtacac cgaatttgcg	600
gtgatcttgt acgcaccctg cgcaacgtcg tgcatcatat actcgatcga atccttgtca	660
tactttcccg cctcgctgcg gtgaaattta cgattctca acgcctcctt tataatcgaa	720
gacgtgaggt tttcttggg c atg ggt acc agc aac aag tcc cca tta ctt Met Gly Thr Ser Asn Lys Ser Pro Leu Leu	771
1 5 10	
tcc acc gca atg ttg ttg ggg caa acg cgc tca gcg agc ata atc gaa Ser Thr Ala Met Leu Leu Gly Gln Thr Arg Ser Ala Ser Ile Ile Glu	819
15 20 25	
ggg tac agc gaa tta aag tcc ata atc acc aaa tgt tcg tgc agt ccc Gly Tyr Ser Glu Leu Lys Ser Ile Ile Thr Lys Cys Ser Cys Ser Pro	867
30 35 40	
ggc acc gtt gga agc acc agt cca cct cca att tta gtg tta ccc tgg Gly Thr Val Gly Ser Thr Ser Pro Pro Ile Leu Val Leu Pro Trp	915
45 50 55	
tca ccc caa gtt tgc tgt gcg gtc gag ata cga aac aac gat tta cgc Ser Pro Gln Val Cys Cys Ala Val Glu Ile Arg Asn Asn Asp Leu Arg	963
60 65 70	
tcc agg tca tcg agc tcg tct tgg cgc tcc ggt gaa cgt tta cgc tcc Ser Arg Ser Ser Ser Trp Arg Ser Gly Glu Arg Leu Arg Ser	1011
75 80 85 90	
tcc tcg atg gca cgc ttg aac gat atg ttt aaa att tcc gca tca Ser Ser Met Ala Arg Leu Asn Asp Met Phe Lys Ile Ser Ala Ser	1056
95 100 105	
taacgttgcc tccggccacc caaaaacctcg ggcgaaagggt tttgcgcag cgaatccgt	1116
aagggttaaa tttggttcat ctgcggccca cggtaaaaaga acaaagtgtt gtacgcctt	1176
acggcacccct cgtccagcgc ataattcatc gtgttaaccgg tcatacgtgc cttggtaag	1236
agccgttccg ggcgttggag gtgcagcgcg agcattgtca caaaaattgc atccaccatg	1296
ttataactcga tgatgagtg tggctgtccc tgctcgtagt ccactttcat cactttaaa	1356
tcataactaa ttttcttcgc accgaggtac ttggaggcca ggtcgtccag cttgaagct	1416
gtttcgccgg ggtgccactt gcccggaaac ttgaacatgt ccagcatttgc ttaggacgag	1476
ctgggtatgc ggttacgtc aacgtacgag tcattcttta caaaattaat cgtcgatca	1536
gtgacaccgt atcgataaa ctgtacgtc tttagctcg ggtcaccact ttggcggtgt	1596
atcatgtacg gtatatcgta gccgtgtccg taaaagtcca ccaccaggc cgggttgagg	1656
gcgtcaatca gcgttataaa gtttccatc agttcagttt catccttgc caaaatgacc	1716
ctaattgggg taccctccctt gaacgtgtcc accgtggcc ggtactcgct atcgatgacc	1776
gcattcgggt ccaggtagag ttgaaaatat tctgtcacct cggcgctctc gtatgtga	1836
atg gaa atg gag aaa act gta tca ccc tcg atg gtg ggg tcg gcc atg Met Glu Met Glu Lys Thr Val Ser Pro Ser Met Val Gly Ser Ala Met	1884
110 115 120	
cgg tgg tgc ttg gaa cta tta tac gtt tct ata tcg tac gag gcc ata	1932

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Arg Trp Cys Leu Glu Leu Leu Tyr Val Ser Ile Ser Tyr Glu Ala Ile		
125	130	135
gtc atc ttg atg ggc ttc agc ggc acc agt tgg tca tcg gtc atc ttt		1980
Val Ile Leu Met Gly Phe Ser Gly Thr Ser Trp Ser Ser Val Ile Phe		
140	145	150
ttg ggg cca cgc gga ttg taggcaattt gaaaccggtt cacccctcg		2028
Leu Gly Pro Arg Gly Leu		
155		
ggtagagcaa gcgttggcac gttaaacctgg gcgtatgtta gcccacgtac ggtccccattt		2088
tgcggcgtga ggtgggttgtt gaaggccaca taactggatt caaaaatttt ataataattc		2148
atgaacacctc cgacgtccga catgttgaa tcgcacagat agttccctcac accgtttgtta		2208
gtctggcgaa cccgttttat caccgggttg atgtggtccg gtgcgaggac cggtgtgcat		2268
ggtacgcaca gtttacagtc aacccgcacc tttcttcac agttgcagaa ggcgtacccc		2328
acgattggta cactgtacag gatcacctt attccgatga agggattgcg cagatagagg		2388
tgcacccgc tcgggttag atagctgttc ggacgctcg ctgagatgcg ccgaatcttg		2448
gtaataagga atacggcggtt ggccggtaca gtgttattcg accgtgtaga gtccacatag		2508
ttgcgcaccc cctccaggaa acatttcttc ataaac atg gct gaa gtg cac aat		2562
Met Ala Glu Val His Asn		
160	165	
gtg gtg aga cca acc gtg tcg gct cta act gcg tac cgt tta cag		2610
Val Val Val Arg Pro Thr Val Ser Ala Leu Thr Ala Tyr Arg Leu Gln		
170	175	180
cgc gtg aat cgt gat ttg gaa aca aaa gta tcg cga atg gcg cag cac		2658
Arg Val Asn Arg Asp Leu Glu Thr Lys Val Ser Arg Met Ala Gln His		
185	190	195
tct agc gcg gaa ccg ttt atc agg cag act ttg ata cgt gaa ctg gga		2706
Ser Ser Ala Glu Pro Phe Ile Arg Gln Thr Leu Ile Arg Glu Leu Gly		
200	205	210
gac ttg cga gat gct gaa caa ata ccc acc acg tcc ctg ttg gat ctt		2754
Asp Leu Arg Asp Ala Glu Gln Ile Pro Thr Thr Ser Leu Leu Asp Leu		
215	220	225
ttt atc acc cga acc aac gct gag aag gag agt tta cgg ctc ggt gta		2802
Phe Ile Thr Arg Thr Asn Ala Glu Lys Ser Leu Arg Leu Gly Val		
230	235	240
245		
act atg tcg ggc gaa gag gta tcg cga atg aat gaa aac ttt att caa		2850
Thr Met Ser Gly Glu Val Ser Arg Met Asn Glu Asn Phe Ile Gln		
250	255	260
cga ttt cgc tcc aac aag gac aat gaa gct gag gcc gaa ggt gca gtg		2898
Arg Phe Arg Ser Asn Lys Asp Asn Glu Ala Glu Ala Glu Gly Ala Val		
265	270	275
gtg acc ccc aac gaa cgc tta tgt agt act gag ggt gac gtt gaa aag		2946
Val Thr Pro Asn Glu Arg Leu Cys Ser Thr Glu Gly Asp Val Glu Lys		
280	285	290
att gcg atg aac tac cgc tcg gac ctg gtg gcc ata aac cgt gag ctc		2994
Ile Ala Met Asn Tyr Arg Ser Asp Leu Val Ala Ile Asn Arg Glu Leu		
295	300	305
acc cag gcc atc gaa aat ctg agc ccg gga aat gtg gaa acg ttg tac		3042
Thr Gln Ala Ile Glu Asn Leu Ser Pro Gly Asn Val Glu Thr Leu Tyr		
310	315	320
325		
gag cgg ttt gag ttg gtt cgc acc act cta gct cca att cta ccc cgc		3090
Glu Arg Phe Glu Leu Val Arg Thr Thr Leu Ala Pro Ile Leu Pro Arg		
330	335	340
ctt tcg ggg ttg ggt aaa ctg gcg ctt aac gcg ctc ccc ctg ctg tac		3138
Leu Ser Gly Leu Gly Lys Leu Ala Leu Asn Ala Leu Pro Leu Leu Tyr		
345	350	355

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gaa aag acc aac agt gac aac aaa gac gtg ctg aag ttg gac att cgt	3186
Glu Lys Thr Asn Ser Asp Asn Lys Asp Val Leu Lys Leu Asp Ile Arg	
360	365
	370

atc aaa gaa ttc	3198
Ile Lys Glu Phe	
375	

<210> SEQ_ID NO 84
<211> LENGTH: 105
<212> TYPE: PRT
<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 84

Met Gly Thr Ser Asn Lys Ser Pro Leu Leu Ser Thr Ala Met Leu Leu	
1	5
	10
	15

Gly Gln Thr Arg Ser Ala Ser Ile Ile Glu Gly Tyr Ser Glu Leu Lys	
20	25
	30

Ser Ile Ile Thr Lys Cys Ser Cys Ser Pro Gly Thr Val Gly Ser Thr	
35	40
	45

Ser Pro Pro Pro Ile Leu Val Leu Pro Trp Ser Pro Gln Val Cys Cys	
50	55
	60

Ala Val Glu Ile Arg Asn Asn Asp Leu Arg Ser Arg Ser Ser Ser Ser	
65	70
	75
	80

Ser Trp Arg Ser Gly Glu Arg Leu Arg Ser Ser Ser Met Ala Arg Leu	
85	90
	95

Asn Asp Met Phe Lys Ile Ser Ala Ser	
100	105

<210> SEQ_ID NO 85
<211> LENGTH: 54
<212> TYPE: PRT
<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 85

Met Glu Met Glu Lys Thr Val Ser Pro Ser Met Val Gly Ser Ala Met	
1	5
	10
	15

Arg Trp Cys Leu Glu Leu Leu Tyr Val Ser Ile Ser Tyr Glu Ala Ile	
20	25
	30

Val Ile Leu Met Gly Phe Ser Gly Thr Ser Trp Ser Ser Val Ile Phe	
35	40
	45

Leu Gly Pro Arg Gly Leu	
50	

<210> SEQ_ID NO 86
<211> LENGTH: 218
<212> TYPE: PRT
<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 86

Met Ala Glu Val His Asn Val Val Val Arg Pro Thr Val Ser Ala Leu	
1	5
	10
	15

Thr Ala Tyr Arg Leu Gln Arg Val Asn Arg Asp Leu Glu Thr Lys Val	
20	25
	30

Ser Arg Met Ala Gln His Ser Ser Ala Glu Pro Phe Ile Arg Gln Thr	
35	40
	45

Leu Ile Arg Glu Leu Gly Asp Leu Arg Asp Ala Glu Gln Ile Pro Thr	
50	55
	60

Thr Ser Leu Leu Asp Leu Phe Ile Thr Arg Thr Asn Ala Glu Lys Glu	
65	70
	75
	80

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Ser Leu Arg Leu Gly Val Thr Met Ser Gly Glu Glu Val Ser Arg Met
85 90 95

Glu Ala Glu Gly Ala Val Val Thr Pro Asn Glu Arg Leu Cys Ser Thr
 115 120 125

Glu Gly Asp Val Glu Lys Ile Ala Met Asn Tyr Arg Ser Asp Leu Val
 130 135 140

Ala Ile Asn Arg Glu Leu Thr Gln Ala Ile Glu Asn Leu Ser Pro Gly
145 150 155 160

Asn Val Glu Thr Leu Tyr Glu Arg Phe Glu Leu Val Arg Thr Thr Leu
165 170 175

Ala Pro Ile Leu Pro Arg Leu Ser Gly Leu Gly Lys Leu Ala Leu Asn
180 185 190

Ala Leu Pro Leu Leu Tyr Glu Lys Thr Asn Ser Asp Asn Lys Asp Val
195 200 205

Leu Lys Leu Asp Ile Arg Ile Lys Glu Phe
210 215

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<210> SEQ ID NO 87
<211> LENGTH: 3198
<212> TYPE: DNA
<213> ORGANISM: mosquito baculovirus
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (428)...(3195)
<221> NAME/KEY: CDS
<222> LOCATION: (20)...(241)
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<400> SEQUENCE: 87

gaattctttg atacgaatg tcc aac ttc agc acg tct ttg ttg tca ctg ttg 52
 Ser Asn Phe Ser Thr Ser Leu Leu Ser Leu Leu
 1 5 10

```

gtc ttt tcg tac agc agg ggg agc gcg tta agc gcc agt tta ccc aac 100
Val Phe Ser Tyr Ser Arg Gly Ser Ala Leu Ser Ala Ser Leu Pro Asn
          15           20           25

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ccc gaa agg cgg ggt aga att gga gct aga gtg gtg cga acc aac tca      148
Pro Glu Arg Arg Gly Arg Ile Gly Ala Arg Val Val Arg Thr Asn Ser
          30           35           40

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aac cgc tcg tac aac gtt tcc aca ttt ccc ggg ctc aga ttt tcg atg 196
Asn Arg Ser Tyr Asn Val Ser Thr Phe Pro Gly Leu Arg Phe Ser Met
 ⁵⁵ ⁵⁶ ⁵⁷

gcc tgg gtg agc tca cgg ttt atg gcc acc agg tcc gag cgg tag 241
Ala Trp Val Ser Ser Arg Phe Met Ala Thr Arg Ser Glu Arg *

ttcatcgcaa tctttcaac gtcaccctca gtactacata agcgttcggtt gggggtcacc 301

tcatttcattc gcgataccctc ttgcggccgac atagttacac cgagccgtaa actctcccttc 421

```

tcagcg ttg gtt cgg gtg ata aaa aga tcc aac agg gac gtg gtg ggt      469
      Leu Val Arg Val Ile Lys Arg Ser Asn Arg Asp Val Val Gly
      75          80          85

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att tgt tca gca tct cgc aag tct ccc agt tca cgt atc aaa gtc tgc	517	
Ile Cys Ser Ala Ser Arg Lys Ser Pro Ser Ser Arg Ile Lys Val Cys		
90	95	100

```

ctg ata aac ggt tcc gcg cta gag tgc tgc gcc att cgc gat act ttt      565
Leu Ile Asn Gly Ser Ala Leu Glu Cys Cys Ala Ile Arg Asp Thr Phe
    105          110          115

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gtt tcc aaa tca cga ttc acg cgc tgt aaa cggt tac gca gtt aga gcc Val Ser Lys Ser Arg Phe Thr Arg Cys Lys Arg Tyr Ala Val Arg Ala 120 125 130 135	613
gac acg gtt ggt ctc acc acc aca ttg tgc act tca gcc atg ttt atg Asp Thr Val Gly Leu Thr Thr Leu Cys Thr Ser Ala Met Phe Met 140 145 150	661
aag aaa tgt tcc tgg gag gag gtg cgc aac tat gtg gac tct aca cgg Lys Lys Cys Ser Trp Glu Glu Val Arg Asn Tyr Val Asp Ser Thr Arg 155 160 165	709
tgc gaa tac act gta ccg gcc aac gcc ttc ctt att acc aag att Cys Glu Tyr Thr Val Pro Ala Asn Ala Val Phe Leu Ile Thr Lys Ile 170 175 180	757
cgg tgc atc tca gac gag cgt ccg aac agc tat cta caa ccg agc gag Arg Cys Ile Ser Asp Glu Arg Pro Asn Ser Tyr Leu Gln Pro Ser Glu 185 190 195	805
gtg cac ctc tat ctg cgc aat ccc ttc atc gga atc aag gtg atc ctg Val His Leu Tyr Leu Arg Asn Pro Phe Ile Gly Ile Lys Val Ile Leu 200 205 210 215	853
tac agt gta cca atc gtg ggg tac gcc ttc tgc aac tgt gaa aga aag Tyr Ser Val Pro Ile Val Gly Tyr Ala Phe Cys Asn Cys Glu Arg Lys 220 225 230	901
ggc gag gtt gac tgt aaa ctg tgc gta cca tgc aca ccg gtc ctc gca Gly Glu Val Asp Cys Lys Leu Cys Val Pro Cys Thr Pro Val Leu Ala 235 240 245	949
ccg gac cac atc aac ccg gtg ata aag ccg gtt cgc cag act aca aac Pro Asp His Ile Asn Pro Val Ile Lys Arg Val Arg Gln Thr Thr Asn 250 255 260	997
ggt gtg agg aac tat ctg tgc gat tcc aac atg tcg gac gtc gag agg Gly Val Arg Asn Tyr Leu Cys Asp Ser Asn Met Ser Asp Val Glu Arg 265 270 275	1045
ttc atg aat tat tat aaa att ttt gaa tcc agt tat gtg gcc ttc acc Phe Met Asn Tyr Tyr Lys Ile Phe Glu Ser Ser Tyr Val Ala Phe Thr 280 285 290 295	1093
acc cac ctc acg ccg caa aat ggg acc gta cgt ggg cta aac atc gcc Thr His Leu Thr Pro Gln Asn Gly Thr Val Arg Gly Leu Asn Ile Ala 300 305 310	1141
cag gtt tac gtg cca acg ctt gct cta ccc gag gag gtg aac ggg ttt Gln Val Tyr Val Pro Thr Leu Ala Leu Pro Glu Glu Val Asn Gly Phe 315 320 325	1189
caa att gcc tac aat ccg cgt ggc ccc aaa aag atg acc gat gac caa Gln Ile Ala Tyr Asn Pro Arg Gly Pro Lys Lys Met Thr Asp Asp Gln 330 335 340	1237
ctg gtg ccg ctg aag ccc atc aag atg act atg gcc tcg tac gat ata Leu Val Pro Leu Lys Pro Ile Lys Met Thr Met Ala Ser Tyr Asp Ile 345 350 355	1285
gaa acg tat aat agt tcc aag cac cac cgc atg gcc gac ccc acc atc Glu Thr Tyr Asn Ser Lys His His Arg Met Ala Asp Pro Thr Ile 360 365 370 375	1333
gag ggt gat aca gtt ttc tcc att tcc att cac tac tac gag agc gcc Glu Gly Asp Thr Val Phe Ser Ile Ser Ile His Tyr Tyr Glu Ser Ala 380 385 390	1381
gag gtg cag gaa tat ttt caa ctc tac ctg gac ccg aat gcg gtc atc Glu Val Gln Glu Tyr Phe Gln Leu Tyr Leu Asp Pro Asn Ala Val Ile 395 400 405	1429
gat agc gag tac ccg ccc acg gtg gac acg ttc aag gag ggt acc acc Asp Ser Glu Tyr Arg Pro Thr Val Asp Thr Phe Lys Glu Gly Thr Thr 410 415 420	1477
att agg gtc att ttg tgc aag gat gaa gct gaa ctg atg gac aac ttt Ile Arg Val Ile Leu Cys Lys Asp Glu Ala Glu Leu Met Asp Asn Phe 425 430 435	1525

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ata acg ctg att gac gcc ctc aac ccg gac ctg gtg gtg gac ttt aac Ile Thr Leu Ile Asp Ala Leu Asn Pro Asp Leu Val Val Asp Phe Asn 440 445 450 455	1573
gga cac ggc tac gat ata ccg tac atg att aca cgc caa agt ggt gac Gly His Gly Tyr Asp Ile Pro Tyr Met Ile Thr Arg Gln Ser Gly Asp 460 465 470	1621
ccg aag ctg aac acg ttc aag ttt atg cga tac ggt gtc act gat ccg Pro Lys Leu Asn Thr Phe Lys Phe Met Arg Tyr Gly Val Thr Asp Pro 475 480 485	1669
acg att aat ttt gta aag aat gac tcg tac gtt gac gtg aac cgc atc Thr Ile Asn Phe Val Lys Asn Asp Ser Tyr Val Asp Val Asn Arg Ile 490 495 500	1717
acc agc tcg tcc tac caa atg ctg gac atg ttc aag ttt gcc cgc aag Thr Ser Ser Tyr Gln Met Leu Asp Met Phe Lys Phe Ala Arg Lys 505 510 515	1765
tgg cac ccc ggc gaa acc agc ttc aag ctg gac gac ctg gcc tcc aag Trp His Pro Gly Glu Thr Ser Phe Lys Leu Asp Asp Leu Ala Ser Lys 520 525 530 535	1813
tac ctc ggt gcg aag aaa att agt tat gat ttt aaa gtg atg aaa gtg Tyr Leu Gly Ala Lys Ile Ser Tyr Asp Phe Lys Val Met Lys Val 540 545 550	1861
gac tac gag cag gga cga cca cac ctc atc atc gag tat aac atg gtg Asp Tyr Glu Gln Gly Arg Pro His Leu Ile Ile Glu Tyr Asn Met Val 555 560 565	1909
gat gca att ttg gtg aca atg ctc tcg ctg cac ctc caa gcg ccc gaa Asp Ala Ile Leu Val Thr Met Leu Ser Leu His Leu Gln Ala Pro Glu 570 575 580	1957
cgg ctc ttc acc aag gca cgt atg acc ggt tac acg atg aat tat gcg Arg Leu Phe Thr Lys Ala Arg Met Thr Gly Tyr Thr Met Asn Tyr Ala 585 590 595	2005
ctg gac gag ggt gcc gta aag gcg tac aac act ttg ttc ttt tac cgt Leu Asp Glu Gly Ala Val Lys Ala Tyr Asn Thr Leu Phe Phe Tyr Arg 600 605 610 615	2053
ggg ctc gag atg aac caa att tac acc ttt acg gat tcg ctg cgc aac Gly Leu Glu Met Asn Gln Ile Tyr Thr Phe Thr Asp Ser Leu Arg Asn 620 625 630	2101
aaa ctt tcg ccc gag gtt ttg ggt ggc cgg agg caa cgt tat gat gcg Lys Leu Ser Pro Glu Val Leu Gly Arg Arg Gln Arg Tyr Asp Ala 635 640 645	2149
gaa att tta aac ata tcg ttc aag cgt gcc atc gag gag gag cgt aaa Glu Ile Leu Asn Ile Ser Phe Lys Arg Ala Ile Glu Glu Glu Arg Lys 650 655 660	2197
cgt tca ccg gag cgc caa gac gag ctc gat gac ctg gag cgt aaa tcg Arg Ser Pro Glu Arg Gln Asp Glu Leu Asp Asp Leu Glu Arg Lys Ser 665 670 675	2245
ttg ttt cgt atc tcg acc gca cag caa act tgg ggt gac cag ggt aac Leu Phe Arg Ile Ser Thr Ala Gln Gln Thr Trp Gly Asp Gln Gly Asn 680 685 690 695	2293
act aaa att gga ggt gga ctg gtg ctt cca acg gtg ccg gga ctg cac Thr Lys Ile Gly Gly Leu Val Leu Pro Thr Val Pro Gly Leu His 700 705 710	2341
gaa cat ttg gtg att atg gac ttt aat tcg ctg tac cct tcg att atg Glu His Leu Val Ile Met Asp Phe Asn Ser Leu Tyr Pro Ser Ile Met 715 720 725	2389
ctc gct gag cgc gtt tgc ccc aac aac att gcg gtg gaa agt aat ggg Leu Ala Glu Arg Val Cys Pro Asn Asn Ile Ala Val Glu Ser Asn Gly 730 735 740	2437
gac ttg ttg ctg gta ccc atg ccc aaa gaa aac ctc acg tct tcg att Asp Leu Leu Leu Val Pro Met Pro Lys Glu Asn Leu Thr Ser Ser Ile	2485

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745	750	755	
ata aag gag gcg ttg aag aat cgt aaa ttt cac cgc agc gag gcg gca Ile Lys Glu Ala Leu Lys Asn Arg Lys Phe His Arg Ser Glu Ala Ala	760	765	770
775			
aag tat gac aag gat tcg tac gag tat atg atg cac gac gct gcg cag Lys Tyr Asp Lys Asp Ser Tyr Glu Tyr Met Met His Asp Ala Ala Gln	780	785	790
795	800	805	
ggt gcg tac aag atc acc gca aat tcg gtc tac ggt ttc ttt gcg cta Gly Ala Tyr Lys Ile Thr Ala Asn Ser Val Tyr Gly Phe Phe Ala Leu	805	810	815
820			
cgg ttt cca ccg ttg gga aac ttt atc aca aaa act ggc cgc ggt aaa Arg Phe Pro Pro Leu Gly Asn Phe Ile Thr Lys Thr Gly Arg Gly Lys	810	815	820
825	830	835	
gtt cga tca gcg gtc aat tac act acc gag tac tgg aat gag cag tac Val Arg Ser Ala Val Asn Tyr Thr Glu Tyr Trp Asn Glu Gln Tyr	825	830	835
835			
ggc ctg tgc gca ttt ttc gtt tac gga gac acc gat tcg atc atg ttt Gly Leu Cys Ala Phe Phe Val Tyr Gly Asp Thr Asp Ser Ile Met Phe	840	845	850
855			
aaa ttt atg cag ccc acc agc ggt gta acg gtc gac ccg aat gcg ttt Lys Phe Met Gln Pro Thr Ser Gly Val Thr Val Asp Pro Asn Ala Phe	860	865	870
870			
ccc ggt tta att gaa cat ttt tcc gct gga ttg gcg aaa act gtc ggc Pro Gly Leu Ile Glu His Phe Ser Ala Gly Leu Ala Lys Thr Val Gly	875	880	885
885			
gtc ggt tat aat atg gcg ctc gag ttg att gtc cgg tcg tcc gtc ttt Val Gly Tyr Asn Met Ala Leu Glu Leu Ile Val Arg Ser Ser Val Phe	890	895	900
900			
aca cac cgc aaa aag tcg tac gtg ttt cac att gcc gac aat atc tac Thr His Arg Lys Lys Ser Tyr Val Phe His Ile Ala Asp Asn Ile Tyr	905	910	915
915			
aag tat cgg gga ctt ttg gtc ggc aga aat ttg acc aga gca atc gtc Lys Tyr Arg Gly Leu Leu Val Gly Arg Asn Leu Thr Arg Ala Ile Val	920	925	930
935			
cgg tgc tac aag cga tgg atc gag tat acg atg aag ttg tgc gaa gag Arg Cys Tyr Lys Arg Trp Ile Glu Tyr Thr Met Lys Leu Cys Glu Glu	940	945	950
950			
ggc gcc ctt tcg tac agt tta gct acg gat att ttg ctt gaa gat ttg Gly Ala Leu Ser Tyr Ser Leu Ala Thr Asp Ile Leu Leu Glu Asp Leu	955	960	965
965			
cgt aaa att caa gag gag gac ttt acg gtc gac tcg tta tcc cgc aca Arg Lys Ile Gln Glu Glu Asp Phe Ser Val Asp Ser Leu Ser Arg Thr	970	975	980
980			
att acg tac agc ggc aaa agt ggc agc ttg att gtc aa ttc Ile Ser Tyr Ser Gly Lys Ser Gly Ser Leu Ile Ala	985	990	995
995			
<210> SEQ ID NO 88 <211> LENGTH: 73 <212> TYPE: PRT <213> ORGANISM: mosquito baculovirus			3157
<400> SEQUENCE: 88			3198
Ser Asn Phe Ser Thr Ser Leu Leu Ser Leu Leu Val Phe Ser Tyr Ser 1 5 10 15			
Arg Gly Ser Ala Leu Ser Ala Ser Leu Pro Asn Pro Glu Arg Arg Gly 20 25 30			
Arg Ile Gly Ala Arg Val Val Arg Thr Asn Ser Asn Arg Ser Tyr Asn 35 40 45			

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Val Ser Thr Phe Pro Gly Leu Arg Phe Ser Met Ala Trp Val Ser Ser
50 55 60

Arg Phe Met Ala Thr Arg Ser Glu Arg
65 70

<210> SEQ ID NO 89
<211> LENGTH: 922
<212> TYPE: PRT
<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 89

Leu Val Arg Val Ile Lys Arg Ser Asn Arg Asp Val Val Gly Ile Cys
1 5 10 15

Ser Ala Ser Arg Lys Ser Pro Ser Ser Arg Ile Lys Val Cys Leu Ile
20 25 30

Asn Gly Ser Ala Leu Glu Cys Cys Ala Ile Arg Asp Thr Phe Val Ser
35 40 45

Lys Ser Arg Phe Thr Arg Cys Lys Arg Tyr Ala Val Arg Ala Asp Thr
50 55 60

Val Gly Leu Thr Thr Leu Cys Thr Ser Ala Met Phe Met Lys Lys
65 70 75 80

Cys Ser Trp Glu Glu Val Arg Asn Tyr Val Asp Ser Thr Arg Cys Glu
85 90 95

Tyr Thr Val Pro Ala Asn Ala Val Phe Leu Ile Thr Lys Ile Arg Cys
100 105 110

Ile Ser Asp Glu Arg Pro Asn Ser Tyr Leu Gln Pro Ser Glu Val His
115 120 125

Leu Tyr Leu Arg Asn Pro Phe Ile Gly Ile Lys Val Ile Leu Tyr Ser
130 135 140

Val Pro Ile Val Gly Tyr Ala Phe Cys Asn Cys Glu Arg Lys Gly Glu
145 150 155 160

Val Asp Cys Lys Leu Cys Val Pro Cys Thr Pro Val Leu Ala Pro Asp
165 170 175

His Ile Asn Pro Val Ile Lys Arg Val Arg Gln Thr Thr Asn Gly Val
180 185 190

Arg Asn Tyr Leu Cys Asp Ser Asn Met Ser Asp Val Glu Arg Phe Met
195 200 205

Asn Tyr Tyr Lys Ile Phe Glu Ser Ser Tyr Val Ala Phe Thr Thr His
210 215 220

Leu Thr Pro Gln Asn Gly Thr Val Arg Gly Leu Asn Ile Ala Gln Val
225 230 235 240

Tyr Val Pro Thr Leu Ala Leu Pro Glu Glu Val Asn Gly Phe Gln Ile
245 250 255

Ala Tyr Asn Pro Arg Gly Pro Lys Lys Met Thr Asp Asp Gln Leu Val
260 265 270

Pro Leu Lys Pro Ile Lys Met Thr Met Ala Ser Tyr Asp Ile Glu Thr
275 280 285

Tyr Asn Ser Ser Lys His His Arg Met Ala Asp Pro Thr Ile Glu Gly
290 295 300

Asp Thr Val Phe Ser Ile Ser Ile His Tyr Tyr Glu Ser Ala Glu Val
305 310 315 320

Gln Glu Tyr Phe Gln Leu Tyr Leu Asp Pro Asn Ala Val Ile Asp Ser
325 330 335

Glu Tyr Arg Pro Thr Val Asp Thr Phe Lys Glu Gly Thr Thr Ile Arg
340 345 350

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Val Ile Leu Cys Lys Asp Glu Ala Glu Leu Met Asp Asn Phe Ile Thr
355 360 365

Leu Ile Asp Ala Leu Asn Pro Asp Leu Val Val Asp Phe Asn Gly His
370 375 380

Gly Tyr Asp Ile Pro Tyr Met Ile Thr Arg Gln Ser Gly Asp Pro Lys
385 390 395 400

Leu Asn Thr Phe Lys Phe Met Arg Tyr Gly Val Thr Asp Pro Thr Ile
405 410 415

Asn Phe Val Lys Asn Asp Ser Tyr Val Asp Val Asn Arg Ile Thr Ser
420 425 430

Ser Ser Tyr Gln Met Leu Asp Met Phe Lys Phe Ala Arg Lys Trp His
435 440 445

Pro Gly Glu Thr Ser Phe Lys Leu Asp Asp Leu Ala Ser Lys Tyr Leu
450 455 460

Gly Ala Lys Lys Ile Ser Tyr Asp Phe Lys Val Met Lys Val Asp Tyr
465 470 475 480

Glu Gln Gly Arg Pro His Leu Ile Ile Glu Tyr Asn Met Val Asp Ala
485 490 495

Ile Leu Val Thr Met Leu Ser Leu His Leu Gln Ala Pro Glu Arg Leu
500 505 510

Phe Thr Lys Ala Arg Met Thr Gly Tyr Thr Met Asn Tyr Ala Leu Asp
515 520 525

Glu Gly Ala Val Lys Ala Tyr Asn Thr Leu Phe Phe Tyr Arg Gly Leu
530 535 540

Glu Met Asn Gln Ile Tyr Thr Phe Thr Asp Ser Leu Arg Asn Lys Leu
545 550 555 560

Ser Pro Glu Val Leu Gly Arg Arg Gln Arg Tyr Asp Ala Glu Ile
565 570 575

Leu Asn Ile Ser Phe Lys Arg Ala Ile Glu Glu Glu Arg Lys Arg Ser
580 585 590

Pro Glu Arg Gln Asp Glu Leu Asp Asp Leu Glu Arg Lys Ser Leu Phe
595 600 605

Arg Ile Ser Thr Ala Gln Gln Thr Trp Gly Asp Gln Gly Asn Thr Lys
610 615 620

Ile Gly Gly Leu Val Leu Pro Thr Val Pro Gly Leu His Glu His
625 630 635 640

Leu Val Ile Met Asp Phe Asn Ser Leu Tyr Pro Ser Ile Met Leu Ala
645 650 655

Glu Arg Val Cys Pro Asn Asn Ile Ala Val Glu Ser Asn Gly Asp Leu
660 665 670

Leu Leu Val Pro Met Pro Lys Glu Asn Leu Thr Ser Ser Ile Ile Lys
675 680 685

Glu Ala Leu Lys Asn Arg Lys Phe His Arg Ser Glu Ala Ala Lys Tyr
690 695 700

Asp Lys Asp Ser Tyr Glu Tyr Met Met His Asp Ala Ala Gln Gly Ala
705 710 715 720

Tyr Lys Ile Thr Ala Asn Ser Val Tyr Gly Phe Phe Ala Leu Arg Phe
725 730 735

Pro Pro Leu Gly Asn Phe Ile Thr Lys Thr Gly Arg Gly Lys Val Arg
740 745 750

Ser Ala Val Asn Tyr Thr Thr Glu Tyr Trp Asn Glu Gln Tyr Gly Leu
755 760 765

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Cys Ala Phe Phe Val Tyr Gly Asp Thr Asp Ser Ile Met Phe Lys Phe
770 775 780

Met Gln Pro Thr Ser Gly Val Thr Val Asp Pro Asn Ala Phe Pro Gly
785 790 795 800

Leu Ile Glu His Phe Ser Ala Gly Leu Ala Lys Thr Val Gly Val Gly
805 810 815

Tyr Asn Met Ala Leu Glu Leu Ile Val Arg Ser Ser Val Phe Thr His
820 825 830

Arg Lys Lys Ser Tyr Val Phe His Ile Ala Asp Asn Ile Tyr Lys Tyr
835 840 845

Arg Gly Leu Leu Val Gly Arg Asn Leu Thr Arg Ala Ile Val Arg Cys
850 855 860

Tyr Lys Arg Trp Ile Glu Tyr Thr Met Lys Leu Cys Glu Glu Gly Ala
865 870 875 880

Leu Ser Tyr Ser Leu Ala Thr Asp Ile Leu Leu Glu Asp Leu Arg Lys
885 890 895

Ile Gln Glu Glu Asp Phe Ser Val Asp Ser Leu Ser Arg Thr Ile Ser
900 905 910

Tyr Ser Gly Lys Ser Gly Ser Leu Ile Ala
915 920

<210> SEQ_ID NO 90
<211> LENGTH: 3198
<212> TYPE: DNA
<213> ORGANISM: mosquito baculovirus
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (667)...(897)

<400> SEQUENCE: 90

gaattcttg atacgaatgt ccaacttcag cacgtcttgc ttgtcactgt tggcttttc	60
gtacagcagg gggagcgcgt taagcgccag ttacccaac cccgaaaggc ggggtagaat	120
tggagctaga gtggtgcgaa ccaactcaaa ccgctcgta aacgtttcca catttcccg	180
gctcagatTT tcgatggcct gggtagctc acggTTTatg gccaccaggC ccgagcggta	240
gttcatcgca atctttcaa cgtcacccctc agtactacat aagcgttcgt tgggggtcac	300
cactgcacct tcggcctcag cttcattgtc ctgttggag cggaaatcggtt gaataaaagtt	360
ttcatttcatt cgcgataacct cttcgcccga catagttaca ccgagccgta aactctccctt	420
ctcagcgTTT gttcggttga taaaaagatc caacaggAAC gtgggtggta ttgttcagc	480
atctcgcaag tctcccaatggtt cacgttatcaa agtctgcgtt ataaacgggtt ccgcgtttaga	540
gtgctgcGCC attcgcgata cttttgtttc caaatcacga ttacgcgcgtt gtAAACGGTA	600
cgcagttaga gcccacacgg ttggtctcac caccacatttgcgttccatgtttat	660
gaagaa atg ttc ctg gga gga ggt gcg caa cta tgt gga ctc tac acg	708
Met Phe Leu Gly Gly Ala Gln Leu Cys Gly Leu Tyr Thr	
1 5 10	
gtg cga ata cac tgt acc ggc caa cgc cgt att cct tat tac caa gat	756
Val Arg Ile His Cys Thr Gly Gln Arg Arg Ile Pro Tyr Tyr Gln Asp	
15 20 25 30	
tcg gtg cat ctc aga cga gcg tcc gaa cag cta tct aca acc gag cga	804
Ser Val His Leu Arg Arg Ala Ser Glu Gln Leu Ser Thr Thr Glu Arg	
35 40 45	
ggt gca cct cta tct gcg caa tcc ctt cat cgg aat caa ggt gat cct	852
Gly Ala Pro Leu Ser Ala Gln Ser Leu His Arg Asn Gln Gly Asp Pro	
50 55 60	

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tggcagctt attgcgaatt c	3198
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<210> SEQ_ID NO 91
<211> LENGTH: 76
<212> TYPE: PRT
<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 91

Met Phe Leu Gly Gly Gly Ala Gln Leu Cys Gly Leu Tyr Thr Val Arg				
1	5		10	15
	10	15		

Ile His Cys Thr Gly Gln Arg Arg Ile Pro Tyr Tyr Gln Asp Ser Val			
20	25		30
	30		

His Leu Arg Arg Ala Ser Glu Gln Leu Ser Thr Thr Glu Arg Gly Ala			
35	40		45
	45		

Pro Leu Ser Ala Gln Ser Leu His Arg Asn Gln Gly Asp Pro Val Gln			
50	55		60
	60		

Cys Thr Asn Arg Gly Val Arg Leu Leu Gln Leu Lys			
65	70		75
	75		

<210> SEQ_ID NO 92
<211> LENGTH: 3198
<212> TYPE: DNA
<213> ORGANISM: mosquito baculovirus
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (696)...(848)

<400> SEQUENCE: 92

gaattcttg atacgaatgt ccaacttcag cacgtctttg ttgtcactgt tggcttttc	60
---	----

gtacagcagg gggagcgcgt taagcgccag tttacccaac cccgaaaggc gggtagaat	120
--	-----

tggagctaga gtggcgcgaa ccaactcaa ccgtcgtac aacgtttcca catttcccg	180
--	-----

gctcagattt tcgatggcct gggtagctc acggtttatg gccaccaggt ccgagcggta	240
--	-----

gttcatcgca atctttcaa cgtcacccctc agtactacat aagcgttcgt tgggggtcac	300
---	-----

cactgcacct tcggcctcag cttcattgtc ctgttggag cgaatcgtt gaataaaagt	360
---	-----

ttcattcatt cgcgataacct cttccccga catagttaca ccgagccgta aactctccctt	420
--	-----

ctcagcgtt gttccgggtga taaaaagatc caacagggac gtgggtggta tttgttcagc	480
---	-----

atctcgcaag tctcccgatt cacgtatcaa agtctgcctg ataaacgggtt ccgcgcgtaga	540
---	-----

gtgctgcgcc attcgcgata cttttgttcc caaatcacga ttcacgcgt gtaaacggta	600
--	-----

cgcagttaga gccgacacgg ttggtctcac caccacattg tgcacttcag ccatgtttat	660
---	-----

gaagaaaatgt tcctgggagg aggtgcgcaa ctatg tgg act cta cac ggt gcg	713
Trp Thr Leu His Gly Ala	
1	5

aat aca ctg tac cgg cca acg ccg tat tcc tta tta cca aga ttc ggt	761		
Asn Thr Leu Tyr Arg Pro Thr Pro Tyr Ser Leu Leu Pro Arg Phe Gly			
10	15		20
	20		

gca tct cag acg agc gtc cga aca gct atc tac aac cga gcg agg tgc	809		
Ala Ser Gln Thr Ser Val Arg Thr Ala Ile Tyr Asn Arg Ala Arg Cys			
25	30		35
	35		

acc tct atc tgc gca atc cct tca tcg gaa tca agg tga tcctgtacag	858		
Thr Ser Ile Cys Ala Ile Pro Ser Ser Glu Ser Arg *			
40	45		50
	50		

tgtaccaatc gtggggtagc ctttctgcaa ctgtgaaaga aagggcgagg ttgactgtaa	918
---	-----

actgtgcgtt ccatgcacac cggcctcgc accggaccac atcaacccgg tgataaaagcg	978
---	-----

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ggttcgccag	actacaaacg	gtgtgaggaa	ctatctgtgc	gattccaaca	tgtcggacgt	1038
cgagaggttc	atgaattattt	ataaaaatttt	tgaatccagt	tatgtggcct	tcaccaccca	1098
cctcacgccc	caaaaatggga	ccgtacgtgg	gctaaacatc	gcccagggtt	acgtgccaac	1158
gcttgctcta	cccgaggagg	tgaacgggtt	tcaaattgcc	tacaatccgc	gtggccccaa	1218
aaagatgacc	gatgaccaac	tggtcccgct	gaagcccata	aagatgacta	tggcctcgta	1278
cgatatacaa	acgtataata	gttccaagca	ccaccgcata	gccgaccctt	ccatcgaggg	1338
tgatacagtt	ttctccattt	ccattcacta	ctacgagac	gccgagggtc	aggaatattt	1398
tcaactctac	ctggaccctga	atgcggcat	cgatagcag	taccggccca	cggggacac	1458
gttcaaggag	ggtaccacca	ttagggcat	tttgtgcaag	gatgaagctg	aactgatgga	1518
caactttata	acgctgattt	acgcctcaa	ccoggacctg	gtgggtggact	ttaacggaca	1578
cggctacgtat	ataccgtaca	tgattacacg	ccaaagggtgt	gacccgaagc	tgaacacgtt	1638
caagtttatg	cgatacgggt	tcactgatcc	gacgattaat	tttgtaaaga	atgactcgta	1698
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cgggtgcgaag	aaaatttagtt	atgattttaa	atgtatgaaa	gtggactacg	agcaggggacg	1878
accacaccc	atcatcgagt	ataacatggt	ggtgcaattt	tttgtgacaa	tgctctcgct	1938
gcacccctcaa	gcccggaaac	ggctcttcac	caaggcacgt	atgaccgggtt	acacgatgaa	1998
ttatgcgctg	gacgagggtg	ccgtaaaggc	gtacaacact	tttgtctttt	accgtgggct	2058
cggatgaac	caaatttaca	ccittacgga	ttcgctgcgc	aacaaacttt	cggccggaggt	2118
tttgggtggc	cggaggcaac	gttatgatgc	ggaaattttt	aacatatcgt	tcaagcgtgc	2178
catcgaggag	gagcgttaaac	ttcacccgga	gcccggaaac	gagctcgatg	acctggagcg	2238
taaatcgtt	tttcgtatct	cgaccgcaca	gcaaaacttgg	ggtgaccagg	gtaacactaa	2298
aattggaggt	ggactgggtc	ttccaaacggt	gccgggactg	cacgaacattt	tttgtgattat	2358
ggactttaat	tcgctgtacc	cttcgattat	gctcgctgag	cgcgtttgcc	ccaacaacat	2418
tgcgggtggaa	agtaatgggg	acttgggtgt	ggtaacccatg	ccaaagaaaa	acccacgtc	2478
ttcgattata	aaggaggcgt	tgaagaatcg	taaatttcac	cgcagcgagg	cgccaaagta	2538
tgacaaggat	tcgtacgagt	atatgtgca	cgacgctgcg	cagggtgcgt	acaagatcac	2598
cgc当地atcg	gtgtacggtt	tcttcgcgt	acggtttcca	ccgttggaa	actttatcac	2658
aaaaactggc	cgc当地atcg	ttcgatcgc	ggtaacattac	actaccgagt	actggaaatga	2718
gcagtgacggc	ctgtgcgcata	tttcgttta	cgagacacc	gattcgatca	tgtttaaatt	2778
tatcgacccc	accagcggt	taacggtgga	ccccaatgcg	tttccgggtt	taattgaaca	2838
ttttccgcgt	ggatggcga	aaactgtggg	cgtcggtat	aatatggcgc	tcgagttgtat	2898
tgtgcggcgt	tccgttta	cacaccgca	aaagtcgtac	gtgtttcaca	ttgcggacaa	2958
tatctacaag	tatcgggac	ttttgggtgg	cagaatttg	accagagcca	tcgtccgggt	3018
ctacaacgca	tggatcgagt	atacgatgaa	gttgtgcgaa	gaggggcccc	tttcgtacag	3078
tttagctacg	gatattttgc	ttgaagattt	gcttaaaattt	caagaggagg	actttacgt	3138
ggactcggtt	tcccgccaa	ttagctacag	cgccaaaagt	ggcagctga	ttgcgaattc	3198

<210> SEQ ID NO 93

<211> LENGTH: 50

<212> TYPE: PRT

<213> ORGANISM: mosquito baculovirus

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<400> SEQUENCE: 93

```

Trp Thr Leu His Gly Ala Asn Thr Leu Tyr Arg Pro Thr Pro Tyr Ser
 1           5          10          15

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Leu Leu Pro Arg Phe Gly Ala Ser Gln Thr Ser Val Arg Thr Ala Ile
 20          25          30

```

```

Tyr Asn Arg Ala Arg Cys Thr Ser Ile Cys Ala Ile Pro Ser Ser Glu
 35          40          45

```

```

Ser Arg
 50

```

<210> SEQ ID NO 94

<211> LENGTH: 6627

<212> TYPE: DNA

<213> ORGANISM: mosquito baculovirus

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (3407)...(5044)

<221> NAME/KEY: CDS

<222> LOCATION: (5065)...(5775)

<221> NAME/KEY: CDS

<222> LOCATION: (1530)...(2066)

<221> NAME/KEY: CDS

<222> LOCATION: (2389)...(2625)

<221> NAME/KEY: CDS

<222> LOCATION: (1)...(237)

<400> SEQUENCE: 94

```

gaa ttc tgc aca ctc gca cca ccc gtt tgc cct ctc caa ctg cac gtt      48
Glu Phe Cys Thr Leu Ala Pro Pro Val Cys Pro Leu Gln Leu His Val
 1           5          10          15

```

```

cgt aca gtg cga tat agt tca gct tgc agc tgg gca cct cgg gga caa      96
Arg Thr Val Arg Tyr Ser Ser Ala Cys Ser Trp Ala Pro Arg Gly Gln
 20          25          30

```

```

tgt gcg gtg aga ggc ctt cac aaa ttt cct gaa tat cgc ggt acg tgt      144
Cys Ala Val Arg Gly Leu His Lys Phe Pro Glu Tyr Arg Gly Thr Cys
 35          40          45

```

```

cgg cga tca act ggt ccc gtt tac cga tac cca ttg cca gct cga tca      192
Arg Arg Ser Thr Gly Pro Val Tyr Arg Tyr Pro Ala Arg Ser
 50          55          60

```

```

gct tca gct tgc act cga gct tca tgc gcc ggt gct cca tat cgg      237
Ala Ser Ala Cys Thr Arg Ala Ser Cys Ala Gly Ala Pro Tyr Arg
 65          70          75

```

```

taatttcaa ttttagactcg tacgattcct gtacgcgcaa ctgttccaac ttgaccactt      297

```

```

tcaattcact attggaccgc gacagggcca actccagctc caaaatctt tcgtttgact      357

```

```

gtagttgatt tgtgggctcc actgcaccctc catcaccctg tccaatggtg ccaatttgca      417

```

```

gctcacctcg ggcacgggcc gctggtaaaa ttttacaaaa cacaagctcc ttgtactttt      477

```

```

gcacattggg cagccgtgaa ccgatcagca tctggtgat tccaccctcg ttgaccacca      537

```

```

caatgtcccg ttcgcgagac gatagctca ccggtgacc ctccagtcgt gctacctctg      597

```

```

attcaacggc acccgaaaaa ggttcggtgt gaactaggc cgacagctt cgcttgaagg      657

```

```

cggcgaggat tcgcgtgtgc gtttggcgat actttcgta acccaagcag cgcgcgtat      717

```

```

ccggccgcccc gaccacggc tcgttggta tcgggtggat gtacaaccgc agcacgacac      777

```

```

tcttgcgtc cacgtccaa ttttgcagct gaaacacgct cgaccccaca tcgcactcca      837

```

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cctcgataat attatcgctc tcgaaaaagt tacagtcaa cgttgcgttc cacagttgc      897

```

```

ttagctgggg ccaaataccc tccttggtgg ccggcagttt ggcgcagtcca tctcgattta      957

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tcatcgctgt ttccatcttc caattgatgg gcaattttac gcacaacccg gcccacaaca      1017

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ccttccactg gatgcgattt cggctggaca ccttgccgca catgctggcc gtgggatcct	1077
tgaagccgag gcccgcgtg acggcgcc cagaaacgta aacctttcca ctgggttgtt	1137
cggtaaagtg gtaaaattgt aacacaagct cagcaccacc gtatcccacc acggtccaca	1197
cttggaaacctt gagctctaga tcgttgcacg ccatgacttc actatccgca ccacacggga	1257
cagctccacc ctttatagc gcataaaccg caacttttag gttaaaaaaa aaaatgatat	1317
taatttttt ataaaaatgga ccgttgagct agagtcacc tcaccacctc acaacctatg	1377
tttccaagtg gcccaattcg gggccggctt gatcatcggt aatttgcgtt gatatgcatt	1437
aaaaaaaaaa acgaatctgg gtttgggggg aaaatatttt tattatttctt accttcaaacc	1497
taaacttcta ccaactgcgg cgactcatca ac atg tcc atc aac cgg agc gac Met Ser Ile Asn Arg Ser Asp	1550
80 85	
gac tgg tgc tgc tgg cac tgg ttc tct aga gtc gga ctc agg ctc agg Asp Trp Cys Cys Trp His Trp Phe Ser Arg Val Gly Leu Arg Leu Arg	1598
90 95 100	
ctc ggg ctt tgg atc ggg ctc ggg ctc gtg ctc gag ttg ggc atc atc Leu Gly Leu Trp Ile Gly Leu Gly Leu Val Leu Glu Leu Gly Ile Ile	1646
105 110 115	
agt tgg cat atc ggg cag ctc tgg tcc cgg ttc agc tgc aga ctc ggg Ser Trp His Ile Gly Gln Leu Trp Ser Arg Phe Ser Cys Arg Leu Gly	1694
120 125 130	
ctc tgg ttt tgg ttc ggg caa atc ttg atc gac tgg ggc tgg act cgg Leu Trp Phe Trp Phe Gly Gln Ile Leu Ile Asp Trp Gly Trp Thr Arg	1742
135 140 145 150	
cgt acg ggc gcg ctt gtt aac cgg ttc gtt tgg ttc aac gac ggt ggt Arg Thr Gly Ala Leu Val Asn Arg Phe Val Trp Phe Asn Asp Gly Gly	1790
155 160 165	
gtc gac cga acg ttt tcc atc tcc aca gcc ttt agg ttt gat aaa gtt Val Asp Arg Thr Phe Ser Ile Ser Ala Phe Arg Phe Asp Lys Val	1838
170 175 180	
cac ctc ggc aat atg ttc acc ggc gcc gaa tgt ggt cgc ttt aag gac His Leu Gly Asn Met Phe Thr Gly Ala Glu Cys Gly Arg Phe Lys Asp	1886
185 190 195	
gta cac ttg cag acg aaa agc gat ctt att gag ctc cgt gcc ctc gcg Val His Leu Gln Thr Lys Ser Asp Leu Ile Glu Leu Arg Ala Leu Ala	1934
200 205 210	
ctg aat cac aaa gac cgc caa att cgg gtt gta att gtg tac ggt cgt Leu Asn His Lys Asp Arg Gln Ile Arg Val Val Ile Val Tyr Gly Arg	1982
215 220 225 230	
gtg cag ctt gat gtc gtg cgg gtg gtc ctc acc aaa ggg tcc act cgt Val Gln Leu Asp Val Val Arg Val Leu Thr Lys Gly Ser Thr Arg	2030
235 240 245	
gct tac ata gtg ata gta cac gtc ggt gag ccc ggg taaaatttagt Ala Tyr Ile Val Ile Val His Val Gly Glu Pro Gly	2076
250 255	
tgggtcgcg atgagatcaa ctgggttaccg ttgctgatct caatctcaa ctgcattgtc	2136
gtatcgaaaca aaaagttctt cgatgttctt cgtaaaaacg ttccacaact cgggactggg	2196
gttgcgtttt ccgcgtatat tctgggtcat agattttaac gacttaatgt ccaccgcctt	2256
atcctaccg tcccccttga taacggtttt gcggtataga aaggaccgtt tgaactgctc	2316
gattggatg cagaagatgt gcctatccat gaccgtcccc gtaacgcgggt tcgtcagttt	2376
acagaccgcc at atg gtc cgg gta gta cgg gca aat gcc aac gct gtg gat Met Val Arg Val Val Arg Ala Asn Ala Asn Ala Val Asp	2427
260 265 270	

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gat ttt cga tgc ggc cat ggt tgg gct gag caa atc gct gtt acc aat Asp Phe Arg Cys Gly His Gly Cys Ala Glu Gln Ile Ala Val Thr Asn 275 280 285	2475
cag gca ggt tac gag cgt gat ggc aat caa cac ggc cct gta gta gcg Gln Ala Gly Tyr Glu Arg Asp Gly Asn Gln His Gly Pro Val Val Ala 290 295 300	2523
gta att tac tat cac ctc gtc cag tgg gta gcc gcg cga gac cag Val Ile Tyr Tyr His Leu Val Val Gln Trp Val Ala Ala Arg Asp Gln 305 310 315	2571
tgg gta ctc gag atc ttc aac gaa ggg gtt tat aat gag gag gtc ctg Trp Val Leu Glu Ile Phe Asn Glu Gly Val Tyr Asn Glu Glu Val Leu 320 325 330 335	2619
tgg tgc tagcaccgca gattccgcgc taacgtacaa ctctagcgcc gagttggcg Trp Cys	2675
aaataaaaat ttgttatctt agcgttctgt atatgcggtc aagttcatcg taaacgtggc caatgtttat aactctaccc ccaaagctgg agcggAACAG gtccagggtcg aaccgcagca	2735 2795
cacaatttgcgttggac gcgtataaac acggcgtcaac tgtacctcg ttttccctgc acatgcccattt cagggccaca taatggtgca ccattgttca gttcagggtac cccatcgaga	2855 2915
gttcgggtgac gttagttttt ctgtatggat ttatcacatgg atttttgtat ccacatgcac cggacagggg ttccggccgac cctcgcgacc ggcttggat tttgttgcatt gaaccggccgc taacgtcactt tcggtaaca gggtagggca ttggaccgac cgtgaagtaa	2975 3035 3095
gtgtatccaa ctccatcaact gcaactgcg cgaacttcaa tctccctcg tcccgattt attataaccc ttggccgcag aaaagtctcg gtaaaacgcattt ccatatggaa acaattcgcc tcgttacggc cggttaaacct tacaaggcggt tttagcgttc gccgtttgtt acaatgtccc	3155 3215 3275
gctctgtata cgaactgcgac accgcaccta acgcaaaacaa tgactactt ttcgtatgc gaatggtaa taagacacgt atttgtaaacc tctggcgcc cgtacacggc caggttggat tatacgaactt a atg aat cga agc tcg aga gcc gag ggt cta cgt gaa tcc Met Asn Arg Ser Ser Arg Ala Glu Gly Leu Arg Glu Ser 340 345 350	3335 3395 3445
ggt ggc gtt aaa ggc cgc cca aaa tca cgc gcc act aca acc atc aaa Gly Gly Val Lys Gly Arg Pro Lys Ser Arg Ala Thr Thr Thr Ile Lys 355 360 365	3493
gct ggt aga ccg gtg cgc cca gct cgg cag cga caa gtt gat gaa att Ala Gly Arg Pro Val Arg Pro Ala Arg Gln Gln Val Asp Glu Ile 370 375 380	3541
tta aac caa gat gaa aat gac gat gta gca cca cct gta gcc gag ccc Leu Asn Gln Asp Glu Asn Asp Asp Val Ala Pro Pro Val Ala Glu Pro 385 390 395	3589
cag cta aat ttg gat gat aat gtt tgg acc ggt ggt gct acg agt ggt Gln Leu Asn Leu Asp Asp Asn Val Trp Thr Gly Gly Ala Thr Ser Gly 400 405 410	3637
gat caa aat gtg gcc cca ggt tca ccc acg ggt ccc gtg gca atg tcg Asp Gln Asn Val Ala Pro Gly Ser Pro Thr Gly Pro Val Ala Met Ser 415 420 425 430	3685
gtg ata tcg aag cgt ctc gtg agc gag tgg cac tcg gac gga gaa ggt Val Ile Ser Lys Arg Leu Val Ser Glu Trp His Ser Asp Gly Glu Gly 435 440 445	3733
gag gat gaa ggt ggg cag gat aac gat ccc gag ccc gag tcg gcg gcc Glu Asp Glu Gly Gly Gln Asp Asn Asp Pro Glu Pro Glu Ser Ala Ala 450 455 460	3781
aag gtg gac gac ttt tta ttt ccc gag ctc gag gaa gac gga ccg gac Lys Val Asp Asp Phe Leu Phe Pro Glu Leu Glu Glu Asp Gly Pro Asp 465 470 475	3829

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tcg gtt ggc gga att ggc aac gtt tct ggt tca gtt ttc gaa gtt gtc Ser Val Gly Gly Ile Gly Asn Val Ser Gly Ser Val Phe Glu Val Val 480 485 490	3877
ggt ggt ggc ccc gag ggc gac tat gct gct ggt gag gag gac gaa gta Gly Gly Pro Glu Gly Asp Tyr Ala Ala Gly Glu Asp Glu Val 495 500 505 510	3925
agc aga aat tcg cta aac ttc gac atg gcg tcc gag gtg caa agt act Ser Arg Asn Ser Leu Asn Phe Asp Met Ala Ser Glu Val Gln Ser Thr 515 520 525	3973
gat gcc gct aag gtg atg gag ctg ttt agc gcc cta tcc gag gag cag Asp Ala Ala Lys Val Met Glu Leu Phe Ser Ala Leu Ser Glu Glu Gln 530 535 540	4021
cga aat gtg att cta aac aac ttt ggt gcg gca cca tcc ggt agc gga Arg Asn Val Ile Leu Asn Asn Phe Gly Ala Ala Pro Ser Gly Ser Gly 545 550 555	4069
acc aca ccg cca acc tcg gtc caa ccc gat atg gag gtt gag gat gtt Thr Thr Pro Pro Thr Ser Ala Gln Pro Asp Met Glu Val Glu Asp Val 560 565 570	4117
gag act gtg gaa aag ccg gag aat tta aac gac att att acg gac cag Glu Thr Val Glu Lys Pro Glu Asn Leu Asn Asp Ile Ile Thr Asp Gln 575 580 585 590	4165
ttg cgc gat ttc atg gca cag gag ctg aaa aag gcc gct gaa aat tat Leu Arg Asp Phe Met Ala Gln Glu Leu Lys Lys Ala Ala Glu Asn Tyr 595 600 605	4213
gta cca aag tgg ggc tca acg gtt ggt gag tcg aaa agt gcg ctc gca Val Pro Lys Trp Gly Ser Thr Val Gly Glu Ser Lys Ser Ala Leu Ala 610 615 620	4261
att acg gtt gcc gat cgc gtg agc aga tcg ttc atg tac gag ggt cgt Ile Thr Val Ala Asp Arg Val Ser Arg Ser Phe Met Tyr Glu Gly Arg 625 630 635	4309
att gtc gac tat aac cag gtt gtg cta cac ata ctg gac aat tat gac Ile Val Asp Tyr Asn Gln Val Val Leu His Ile Leu Asp Asn Tyr Asp 640 645 650	4357
caa agg ttg gag gag ctg ctc tcg ttc cgc acg aaa acc tac ata atc Gln Arg Leu Glu Glu Leu Leu Ser Phe Arg Thr Lys Thr Tyr Ile Ile 655 660 665 670	4405
gcc gaa ggt gta ccg cac gac tcg aag gtg cac gac tat gtg gac ctg Ala Glu Gly Val Pro His Asp Ser Lys Val His Asp Tyr Val Asp Leu 675 680 685	4453
acc cag tat cgg gaa acc gtg ccg tat tca att gcc ctc aac aac ctg Thr Gln Tyr Arg Glu Thr Val Pro Tyr Ser Ile Ala Leu Asn Asn Leu 690 695 700	4501
agc cgc ggt gtg gac cag gcc aac acg ctc cag ttg gcc gag ggg tgc Ser Arg Gly Val Asp Gln Ala Asn Thr Leu Gln Leu Ala Glu Gly Cys 705 710 715	4549
ttg gag cag ctg aat atg gca aaa att ttc aaa gat ttc aac gaa aac Leu Glu Gln Leu Asn Met Ala Lys Ile Phe Lys Asp Phe Asn Glu Asn 720 725 730	4597
att gtg ccc aac aac ctg cac aag cac aag ccc acc ttc ttc tat gcg Ile Val Pro Asn Asn Leu His Lys His Pro Thr Phe Phe Tyr Ala 735 740 745 750	4645
aaa att atg aag ctg ttt gca cga ctg gtg gat agg gtg gac aat gag Lys Ile Met Lys Leu Phe Ala Arg Leu Val Asp Arg Val Asp Asn Glu 755 760 765	4693
acg atg act gcg gtc gag aag cgt ttg ttt cta atg tca caa cgg ttg Thr Met Thr Ala Val Glu Lys Arg Leu Phe Leu Met Ser Gln Arg Leu 770 775 780	4741
atc cat tgt atc cca ctg gta ata atc ggt cta acg ttc gcc tcc aag Ile His Cys Ile Pro Leu Val Ile Ile Gly Leu Thr Phe Ala Ser Lys 785 790 795	4789

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tac cgc acc tcg aag ata gac tgc gaa gct ttg gcc ctg tac gcc gtg Tyr Arg Thr Ser Lys Ile Asp Cys Glu Ala Leu Ala Leu Tyr Ala Val 800 805 810	4837
aac cat gcg ctg tct gaa aag gtg gat aaa ttg ttc aca ttt gcg gaa Asn His Ala Leu Ser Glu Lys Val Asp Lys Leu Phe Thr Phe Ala Glu 815 820 825 830	4885
gca cag tac ggt gaa ccg ctg ctc agc cgc cgt ata cta att gaa gag Ala Gln Tyr Gly Glu Pro Leu Leu Ser Arg Arg Ile Leu Ile Glu Glu 835 840 845	4933
cag gcg tat ctg tct ttc ggg aac cac ctc gag cag cgc aac cgc gag Gln Ala Tyr Leu Ser Phe Gly Asn His Leu Glu Gln Arg Asn Arg Glu 850 855 860	4981
ctg aat gtg att ctg gat acc gta ctc aac gcc gta cga aag acg tac Leu Asn Val Ile Leu Asp Thr Val Leu Asn Ala Val Arg Lys Thr Tyr 865 870 875	5029
agg gtg tct aga gtt taagttgaca ccgattaaag atg ggc tgc gac gta acg Arg Val Ser Arg Val Met Gly Cys Asp Val Thr 880 885	5082
ttc acc ttg atc cac gag gta tat tct gag gtt ccc gtc gat gga aag Phe Thr Leu Ile His Glu Val Tyr Ser Glu Val Pro Val Asp Gly Lys 890 895 900 905	5130
cac gtc ccg gtc gaa tat gac cgg tac aaa atc agg tta ttg aag gag His Val Pro Val Glu Tyr Asp Arg Tyr Lys Ile Arg Leu Leu Lys Glu 910 915 920	5178
ctg acg cgt ttc ctg tgc ggt gaa acg gat aag gtt gac ggt gcc acg Leu Thr Arg Phe Leu Cys Gly Glu Thr Asp Lys Val Asp Gly Ala Thr 925 930 935	5226
agt gaa gct aaa gcg gat tgt ggg ggc aag tac acg gat gaa gag cgc Ser Glu Ala Lys Ala Asp Cys Gly Gly Lys Tyr Thr Asp Glu Glu Arg 940 945 950	5274
aag ctg ttt ggg ttt aaa tcg aag cag gtg att gac gat gaa agg ttg Lys Leu Phe Gly Phe Lys Ser Lys Gln Val Ile Asp Asp Glu Arg Leu 955 960 965	5322
tcc agg ctg ctg gag gat aac aag ttg ctg tac tct gcg gtg agt gag Ser Arg Leu Leu Glu Asp Asn Lys Leu Leu Tyr Ser Ala Val Ser Glu 970 975 980 985	5370
cgt gat gcg gcg aaa cgt gag cgc atg gag cag ctg aag cgg gag gaa Arg Asp Ala Ala Lys Arg Glu Arg Met Glu Gln Leu Lys Arg Glu Glu 990 995 1000	5418
atg gag ctc aag agc caa acg cga aga ttg cgc aaa ctg aac cag ggt Met Glu Leu Lys Ser Gln Thr Arg Arg Leu Arg Lys Leu Asn Gln Gly 1005 1010 1015	5466
cgt ttg ctg tcc aag tct gaa aac ttt ctt tcg atg gac ccc aag ttg Arg Leu Leu Ser Lys Ser Glu Asn Phe Leu Ser Met Asp Pro Lys Leu 1020 1025 1030	5514
cgc gac aag ttg atc gat cgc acc gtc ata ttg gaa cca cag tac gac Arg Asp Lys Leu Ile Asp Arg Thr Val Ile Leu Glu Pro Gln Tyr Asp 1035 1040 1045	5562
att ttg gcc ctg tcc gag tat aac gat ttg gta gcg caa aag gat gcc Ile Leu Ala Leu Ser Glu Tyr Asn Asp Leu Val Ala Gln Lys Asp Ala 1050 1055 1060 1065	5610
ctc gag aag tac gaa cga atg tcc aga cga tcg ata aag aat ccg tac Leu Glu Lys Tyr Glu Arg Met Ser Arg Arg Ser Ile Lys Asn Pro Tyr 1070 1075 1080	5658
acc cgc tcc gcc ata aac atc gtt gag cgc cgt gag ggt gcg tca atg Thr Arg Ser Ala Ile Asn Ile Val Glu Arg Arg Glu Gly Ala Ser Met 1085 1090 1095	5706
ttc cgt gag aag cgc gaa aac att att gac aac atc cgc ggt atc Phe Arg Glu Lys Lys Arg Glu Asn Ile Ile Asp Asn Ile Arg Gly Ile	5754

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1100	1105	1110	
gac agt agc gaa agt gta gcg tggatatttt ttgaaatata aatatataaa			5805
Asp Ser Ser Glu Ser Val Ala			
1115	1120		
attaataaat agataataa ataaatgttt ctggttgaaa ttaaccaata tttattatcg			5865
ttgttatcaca cgtacccata gtaattat atataaaaa aagtccaatg taatttattg			5925
ggccctggaa tactttagcg gtggaccagt gctatcatcc ggtgcggggtc gcttcgtac			5985
gggtgaaatg ggtcaattt caccgcgcct ctgcttgcg tacagttccc aggtcatgg			6045
tgggccttct tggaaacgctt tgaggttagac ctgtatgtcg gcctgttgcg tgggtctgtt			6105
gctgcgcaaa tgtccactgg cctgttgcac aattcggatc gagttgatat agttgtgcag			6165
ctggaccatt tcgtacgcta gtaaattttt aacaaggcg ttgttca gtcgcggggtt			6225
ggcgatgtac tcgttccagct caacgggtgg gattcgcgcg aactcgcgtgg tgccggccga			6285
aatggAACCT tcacggcgc ttagtcctc gagcaccagt aggccgaaaga gttgttgcgaa			6345
ctttaccagt atgacgcccc gcaacaatacg gtatgtgaa acgcagggtt ggcagccaa			6405
cgaaatgtac atgtttgcg ccacgttgtg cacaacttgc agtgggtgcg ggcgcacat			6465
gtcattacgt tggcaacaa ttgttgcgc cacctcgcc atgaggtca tcacgtccaa			6525
cagttgtga aaatgttacat cgtaatgtt ggttagtggg accacccgcaa tgggtccaa			6585
ctcgactcc ttggccgcgc tggatgtt ggcacacaaat tc			6627

<210> SEQ_ID NO 95

<211> LENGTH: 79

<212> TYPE: PRT

<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 95

Glu	Phe	Cys	Thr	Leu	Ala	Pro	Pro	Val	Cys	Pro	Leu	Gln	Leu	His	Val
1				5				10			15				

Arg	Thr	Val	Arg	Tyr	Ser	Ser	Ala	Cys	Ser	Trp	Ala	Pro	Arg	Gly	Gln
							20			25			30		

Cys	Ala	Val	Arg	Gly	Leu	His	Lys	Phe	Pro	Glu	Tyr	Arg	Gly	Thr	Cys
							35			40			45		

Arg	Arg	Ser	Thr	Gly	Pro	Val	Tyr	Arg	Tyr	Pro	Leu	Pro	Ala	Arg	Ser
						50			55			60			

Ala	Ser	Ala	Cys	Thr	Arg	Ala	Ser	Cys	Ala	Gly	Ala	Pro	Tyr	Arg	
						65			70			75			

<210> SEQ_ID NO 96

<211> LENGTH: 179

<212> TYPE: PRT

<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 96

Met	Ser	Ile	Asn	Arg	Ser	Asp	Asp	Trp	Cys	Cys	Trp	His	Trp	Phe	Ser
1								10			15				

Arg	Val	Gly	Leu	Arg	Leu	Arg	Leu	Gly	Leu	Trp	Ile	Gly	Leu	Gly	Leu
							20			25			30		

Val	Leu	Glu	Leu	Gly	Ile	Ile	Ser	Trp	His	Ile	Gly	Gln	Leu	Trp	Ser
							35			40			45		

Arg	Phe	Ser	Cys	Arg	Leu	Gly	Leu	Trp	Phe	Trp	Phe	Gly	Gln	Ile	Leu
							50			55			60		

Ile	Asp	Trp	Gly	Trp	Thr	Arg	Arg	Thr	Gly	Ala	Leu	Val	Asn	Arg	Phe
							65			70			75		80

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Val Trp Phe Asn Asp Gly Gly Val Asp Arg Thr Phe Ser Ile Ser Thr
85 90 95

Ala Phe Arg Phe Asp Lys Val His Leu Gly Asn Met Phe Thr Gly Ala
100 105 110

Glu Cys Gly Arg Phe Lys Asp Val His Leu Gln Thr Lys Ser Asp Leu
115 120 125

Ile Glu Leu Arg Ala Leu Ala Leu Asn His Lys Asp Arg Gln Ile Arg
130 135 140

Val Val Ile Val Tyr Gly Arg Val Gln Leu Asp Val Val Arg Val Val
145 150 155 160

Leu Thr Lys Gly Ser Thr Arg Ala Tyr Ile Val Ile Val His Val Gly
165 170 175

Glu Pro Gly

<210> SEQ ID NO 97

<211> LENGTH: 79

<212> TYPE: PRT

<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 97

Met Val Arg Val Val Arg Ala Asn Ala Asn Ala Val Asp Asp Phe Arg
1 5 10 15

Cys Gly His Gly Cys Ala Glu Gln Ile Ala Val Thr Asn Gln Ala Gly
20 25 30

Tyr Glu Arg Asp Gly Asn Gln His Gly Pro Val Val Ala Val Ile Tyr
35 40 45

Tyr His Leu Val Val Gln Trp Val Ala Ala Arg Asp Gln Trp Val Leu
50 55 60

Glu Ile Phe Asn Glu Gly Val Tyr Asn Glu Glu Val Leu Trp Cys
65 70 75

<210> SEQ ID NO 98

<211> LENGTH: 546

<212> TYPE: PRT

<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 98

Met Asn Arg Ser Ser Arg Ala Glu Gly Leu Arg Glu Ser Gly Gly Val
1 5 10 15

Lys Gly Arg Pro Lys Ser Arg Ala Thr Thr Thr Ile Lys Ala Gly Arg
20 25 30

Pro Val Arg Pro Ala Arg Gln Arg Gln Val Asp Glu Ile Leu Asn Gln
35 40 45

Asp Glu Asn Asp Asp Val Ala Pro Pro Val Ala Glu Pro Gln Leu Asn
50 55 60

Leu Asp Asp Asn Val Trp Thr Gly Gly Ala Thr Ser Gly Asp Gln Asn
65 70 75 80

Val Ala Pro Gly Ser Pro Thr Gly Pro Val Ala Met Ser Val Ile Ser
85 90 95

Lys Arg Leu Val Ser Glu Trp His Ser Asp Gly Glu Gly Glu Asp Glu
100 105 110

Gly Gly Gln Asp Asn Asp Pro Glu Pro Glu Ser Ala Ala Lys Val Asp
115 120 125

Asp Phe Leu Phe Pro Glu Leu Glu Glu Asp Gly Pro Asp Ser Val Gly
130 135 140

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Gly Ile Gly Asn Val Ser Gly Ser Val Phe Glu Val Val Gly Gly Gly
145 150 155 160

Pro Glu Gly Asp Tyr Ala Ala Gly Glu Glu Asp Glu Val Ser Arg Asn
165 170 175

Ser Leu Asn Phe Asp Met Ala Ser Glu Val Gln Ser Thr Asp Ala Ala
180 185 190

Lys Val Met Glu Leu Phe Ser Ala Leu Ser Glu Glu Gln Arg Asn Val
195 200 205

Ile Leu Asn Asn Phe Gly Ala Ala Pro Ser Gly Ser Gly Thr Thr Pro
210 215 220

Pro Thr Ser Ala Gln Pro Asp Met Glu Val Glu Asp Val Glu Thr Val
225 230 235 240

Glu Lys Pro Glu Asn Leu Asn Asp Ile Ile Thr Asp Gln Leu Arg Asp
245 250 255

Phe Met Ala Gln Glu Leu Lys Lys Ala Ala Glu Asn Tyr Val Pro Lys
260 265 270

Trp Gly Ser Thr Val Gly Glu Ser Lys Ser Ala Leu Ala Ile Thr Val
275 280 285

Ala Asp Arg Val Ser Arg Ser Phe Met Tyr Glu Gly Arg Ile Val Asp
290 295 300

Tyr Asn Gln Val Val Leu His Ile Leu Asp Asn Tyr Asp Gln Arg Leu
305 310 315 320

Glu Glu Leu Leu Ser Phe Arg Thr Lys Thr Tyr Ile Ile Ala Glu Gly
325 330 335

Val Pro His Asp Ser Lys Val His Asp Tyr Val Asp Leu Thr Gln Tyr
340 345 350

Arg Glu Thr Val Pro Tyr Ser Ile Ala Leu Asn Asn Leu Ser Arg Gly
355 360 365

Val Asp Gln Ala Asn Thr Leu Gln Leu Ala Glu Gly Cys Leu Glu Gln
370 375 380

Leu Asn Met Ala Lys Ile Phe Lys Asp Phe Asn Glu Asn Ile Val Pro
385 390 395 400

Asn Asn Leu His Lys His Lys Pro Thr Phe Phe Tyr Ala Lys Ile Met
405 410 415

Lys Leu Phe Ala Arg Leu Val Asp Arg Val Asp Asn Glu Thr Met Thr
420 425 430

Ala Val Glu Lys Arg Leu Phe Leu Met Ser Gln Arg Leu Ile His Cys
435 440 445

Ile Pro Leu Val Ile Ile Gly Leu Thr Phe Ala Ser Lys Tyr Arg Thr
450 455 460

Ser Lys Ile Asp Cys Glu Ala Leu Ala Leu Tyr Ala Val Asn His Ala
465 470 475 480

Leu Ser Glu Lys Val Asp Lys Leu Phe Thr Phe Ala Glu Ala Gln Tyr
485 490 495

Gly Glu Pro Leu Leu Ser Arg Arg Ile Leu Ile Glu Glu Gln Ala Tyr
500 505 510

Leu Ser Phe Gly Asn His Leu Glu Gln Arg Asn Arg Glu Leu Asn Val
515 520 525

Ile Leu Asp Thr Val Leu Asn Ala Val Arg Lys Thr Tyr Arg Val Ser
530 535 540

Arg Val
545

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<210> SEQ ID NO 99
<211> LENGTH: 237
<212> TYPE: PRT
<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 99

Met Gly Cys Asp Val Thr Phe Thr Leu Ile His Glu Val Tyr Ser Glu
 1           5          10          15

Val Pro Val Asp Gly Lys His Val Pro Val Glu Tyr Asp Arg Tyr Lys
 20          25          30

Ile Arg Leu Leu Lys Glu Leu Thr Arg Phe Leu Cys Gly Glu Thr Asp
 35          40          45

Lys Val Asp Gly Ala Thr Ser Glu Ala Lys Ala Asp Cys Gly Gly Lys
 50          55          60

Tyr Thr Asp Glu Glu Arg Lys Leu Phe Gly Phe Lys Ser Lys Gln Val
 65          70          75          80

Ile Asp Asp Glu Arg Leu Ser Arg Leu Leu Glu Asp Asn Lys Leu Leu
 85          90          95

Tyr Ser Ala Val Ser Glu Arg Asp Ala Ala Lys Arg Glu Arg Met Glu
100         105         110

Gln Leu Lys Arg Glu Glu Met Glu Leu Lys Ser Gln Thr Arg Arg Leu
115         120         125

Arg Lys Leu Asn Gln Gly Arg Leu Leu Ser Lys Ser Glu Asn Phe Leu
130         135         140

Ser Met Asp Pro Lys Leu Arg Asp Lys Leu Ile Asp Arg Thr Val Ile
145         150         155         160

Leu Glu Pro Gln Tyr Asp Ile Leu Ala Leu Ser Glu Tyr Asn Asp Leu
165         170         175

Val Ala Gln Lys Asp Ala Leu Glu Lys Tyr Glu Arg Met Ser Arg Arg
180         185         190

Ser Ile Lys Asn Pro Tyr Thr Arg Ser Ala Ile Asn Ile Val Glu Arg
195         200         205

Arg Glu Gly Ala Ser Met Phe Arg Glu Lys Lys Arg Glu Asn Ile Ile
210         215         220

Asp Asn Ile Arg Gly Ile Asp Ser Ser Glu Ser Val Ala
225         230         235

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<210> SEQ ID NO 100
<211> LENGTH: 6627
<212> TYPE: DNA
<213> ORGANISM: mosquito baculovirus
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (2159)....(2398)
<221> NAME/KEY: CDS
<222> LOCATION: (402)....(626)
<221> NAME/KEY: CDS
<222> LOCATION: (3200)....(3403)
<221> NAME/KEY: CDS
<222> LOCATION: (3738)....(3923)
<221> NAME/KEY: CDS
<222> LOCATION: (2878)....(3045)

<400> SEQUENCE: 100

gaattctgca cactcgacc acccggttgc cctctccaac tgcacgttcg tacagtgcga      60
tatagttcag cttgcagctg ggcacctcgg ggacaatgtg cggtgagagg ctttcacaaa     120
tttcctgaat atcgcggta cgtgtggcga tcaactggtc ccgtttaccg ataccattg     180
ccagctcgat cagcttcagc ttgcactcga gcttcatcgcg ccgggtgtcc atatcgtaa    240

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tttcaattt agactcgta gattcctgta cgccaaactg ttccaaactt accacattca 300
attcaattt ggaccgcgac agggccaaact ccagctccaa aatctttcg tttgactgtta 360
gttggattgt gggctccact gcacccat caccctgtcc a atg gtg cca att tgc
Met Val Pro Ile Cys
1 5
agc tca cct cgg gca cgg gcc gct ggt aaa att tta cca aac aca agc 464
Ser Ser Pro Arg Ala Arg Ala Gly Lys Ile Leu Pro Asn Thr Ser
10 15 20
tcc ttg tac ttt tgc aca ttg ggc agc cgt gaa ccg atc agc atc tgg 512
Ser Leu Tyr Phe Cys Thr Leu Gly Ser Arg Glu Pro Ile Ser Ile Trp
25 30 35
tgg att cca ccc tcg ttg acc acc aca atg tcc cgt tcg cga gac gat 560
Trp Ile Pro Pro Ser Leu Thr Thr Met Ser Arg Ser Arg Asp Asp
40 45 50
agc tcc acc ggt gca ccc tcc agt cgt gct acc tct gat tca acg gta 608
Ser Ser Thr Gly Ala Pro Ser Ser Arg Ala Thr Ser Asp Ser Thr Val
55 60 65
ccc gaa aaa ggt tcg gtg tgaacttaggt ccgacagctt tcgcttgaag 656
Pro Glu Lys Gly Ser Val
70 75
gcggcgagga ttccgcgttg cgttggcga tactttcgta aacccaagca gcgcgctaga 716
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ctcttcgtcg ccacgtccccca atttgcagc tgaaacacgc tcgacccac atgcactcc 836
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ctgggttaccg ttgcgtatctt caatctcaaa ctgcattgtc gtatcgaaaca aaaaggttct 2156
cq atq ttc ttc qta aaa acq ttc cac aac tcq qqa ctq qgg ttq cqc 2203

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Met Phe Phe Val Lys Thr Phe His Asn Ser Gly Leu Gly Leu Arg		
80	85	90
ttt ccg cgt ata ttc tgg gtc ata gat ttt aac gac tta atg tcc acc	2251	
Phe Pro Arg Ile Phe Trp Val Ile Asp Phe Asn Asp Leu Met Ser Thr		
95	100	105
gcc tta tcc tca ccg tcc cgc ttg ata acg gtt ttg ccg tat aga aag	2299	
Ala Leu Ser Ser Pro Ser Arg Leu Ile Thr Val Leu Arg Tyr Arg Lys		
110	115	120
gac cgt ttg aac tgc tcg att ggg atg cag aag atg tgc cta tcc atg	2347	
Asp Arg Leu Asn Cys Ser Ile Gly Met Gln Lys Met Cys Leu Ser Met		
125	130	135
acc gtc ccc gta acg cgg ttc gtc agt tta cag acc gcc ata tgg tcc	2395	
Thr Val Pro Val Thr Arg Phe Val Ser Leu Gln Thr Ala Ile Trp Ser		
140	145	150
ggg tagtacgggc aaatgccaac gctgtggatg atttcgatg cggccatgg	2448	
Gly		
155		
tgtgctgagc aaatcgctgt taccaatcag gcaggttacg agcgtgatgg caatcaacac	2508	
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gttggacgcg tataaacagg cgtcaactgt acctcggtt tccctgcaca tgcccacat	2868	
ggccacata atg gtg cac cat gtt cga gtt cag gta ccc cat cga gag ttc	2919	
Met Val His Val Arg Val Gln Val Pro His Arg Glu Phe		
160	165	
ggt gac gtg agt ttt gct gta gtt ttt gat gaa aat ttt aca ctt gat	2967	
Gly Asp Val Ser Phe Ala Val Val Phe Asp Glu Asn Phe Thr Leu Asp		
170	175	180
185		
ttt tgt atc cac atg cac cgg aca ggg gtt ccg ccg acc ctc gcg acc	3015	
Phe Cys Ile His Met His Arg Thr Gly Val Pro Pro Thr Leu Ala Thr		
190	195	200
ggc ttg gga ttt tgt tcg atg aac cgc cgc taacgtcagc ttccgttaaca	3065	
Gly Leu Gly Phe Cys Ser Met Asn Arg Arg		
205	210	
gggtgaggca tttgaccgac cgtgaagtaa gtgtatccaa ctccatcaact gcaaactg	3125	
cgaacttcaa tctccctcgat ctcggattt attataaccc ttggccgcag aaaagtctcg	3185	
gtaaacgcat ccat atg gaa aca att cgc ctc gtt acg gcc ggt aaa cct	3235	
Met Glu Thr Ile Arg Leu Val Thr Ala Gly Lys Pro		
215	220	
tac aag cgg ttt gag cag tcg ccg ttt gtt aca atg tcc cgc tct gaa	3283	
Tyr Lys Arg Phe Glu Gln Ser Pro Phe Val Thr Met Ser Arg Ser Glu		
225	230	235
tac gaa ctg cga acc gca cct aac gca aac aat gac tac tct ttc gtg	3331	
Tyr Glu Leu Arg Thr Ala Pro Asn Ala Asn Asn Asp Tyr Ser Phe Val		
240	245	250
255		
atg cga atg ggt aat aag aca cgt att gtg aac ctc tgg gcg ccc gta	3379	
Met Arg Met Gly Asn Lys Thr Arg Ile Val Asn Leu Trp Ala Pro Val		
260	265	270
cac ggc cag gtt tta tac gac taaatgaatc gaagctcagc agccgagggt	3433	
His Gly Gln Val Val Leu Tyr Asp		
275		
ctacgtaat ccgggtggcgt taaaggccgc cccaaatcac gcccactac aaccatcaa	3493	

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gctggtagac cggtgcgccc agctcggcag cgacaagttt atgaaattt aaaccaagat	3553
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tggaccggtg gtgtacgag tggtagatcaa aatgtggccc cagggttcacc cacgggtccc	3673
gtggcaatgt cggtagatatac gaagcgtctc gtgagcgagt ggactcgga cggagaaggt	3733
gagg atg aag gtg ggc agg ata acg atc ccg agc ccg agt ccg cgg cca Met Lys Val Gly Arg Ile Thr Ile Pro Ser Pro Ser Arg Arg Pro 280 285 290	3782
agg tgg acg act ttt tat ttc ccg agc tcg agg aag acg gac ccg act Arg Trp Thr Thr Phe Tyr Phe Pro Ser Ser Arg Lys Thr Asp Arg Thr 295 300 305 310	3830
cgg ttg gcg gaa ttg gca acg ttt ctg gtt cag ttt tcg aag ttg tcg Arg Leu Ala Glu Leu Ala Thr Phe Leu Val Gln Phe Ser Lys Leu Ser 315 320 325	3878
gtg gtg gcc ccg agg gcg act atg ctg ctg gtg agg agg acg aag Val Val Ala Pro Arg Ala Thr Met Leu Leu Val Arg Arg Thr Lys 330 335 340	3923
taagcagaaa ttctgttaaac ttctgacatgg cgtccgaggt gcaaaagtact gatgccgcta	3983
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aggtttaggta tggtagact gtggaaaagc cgagaaattt aaacgacattt attacggacc	4163
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atttcaacga aaacattgtg cccaaacaacc tgcacaagca caagcccacc ttcttctatg	4643
cgaaaattat gaagctgttt gcacgactgg tggatagggt ggacaatgag acgtatgactg	4703
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tggaaagcac gtcccggtcg aatatgaccg gtacaaaatc aggttatttgc aggagctgac	5183
gcgtttctgt tgcgttgcgaa cggataagggt tgcgttgc acgagtgttgc ctaaagcgaa	5243
ttgtgggggc aagtacacgg atgaagagcg caagctgtttt gggttttat cgaagcagggt	5303
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gagttagcgat gatgcggcga aacgtgagcg catggagcg ctgaagcggg aggaaatgg	5423
gctcaagagc caaacgcgaa gattgcgcaaa actgaaccag ggtcgatcc tgcgttgc tgcgttgc	5483
tgaaaacttt ctgtcgatgg accccaaatgtt ggcgttgc gatgtcgatc gcaccgtcat	5543
attggaaacca cgtacgaca tttttggccctt gtcgttgcgtt aacgattttgg tagcgcaaaa	5603

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ctccgcata aacatcggtt agcgcgtga gggtgcgta atgttccgtg agaagaagcg 5723
cgaaaacatt attgacaaca tccgcggtat cgacagtagc gaaaagtgtag cgtatataat 5783
ttttgaaata taaatatata aaattaataa atagataaaat aaataaatgt ttctgggtga 5843
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cggcctgttc gatgggtctg ttgtcgca aatgtccact ggctgttgtt acaattcggt 6143
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atcc 6627

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<210> SEQ ID NO 101

<211> LENGTH: 75

<212> TYPE: PRT

<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 101

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Met Val Pro Ile Cys Ser Ser Pro Arg Ala Arg Ala Ala Gly Lys Ile
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Leu Pro Asn Thr Ser Ser Leu Tyr Phe Cys Thr Leu Gly Ser Arg Glu
20 25 30

Pro Ile Ser Ile Trp Trp Ile Pro Pro Ser Leu Thr Thr Met Ser
35 40 45

Arg Ser Arg Asp Asp Ser Ser Thr Gly Ala Pro Ser Ser Arg Ala Thr
50 55 60

Ser Asp Ser Thr Val Pro Glu Lys Gly Ser Val
65 70 75

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<210> SEQ ID NO 102

<211> LENGTH: 80

<212> TYPE: PRT

<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 102

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Met Phe Phe Val Lys Thr Phe His Asn Ser Gly Leu Gly Leu Arg Phe
1 5 10 15

Pro Arg Ile Phe Trp Val Ile Asp Phe Asn Asp Leu Met Ser Thr Ala
20 25 30

Leu Ser Ser Pro Ser Arg Leu Ile Thr Val Leu Arg Tyr Arg Lys Asp
35 40 45

Arg Leu Asn Cys Ser Ile Gly Met Gln Lys Met Cys Leu Ser Met Thr
50 55 60

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Val Pro Val Thr Arg Phe Val Ser Leu Gln Thr Ala Ile Trp Ser Gly
65 70 75 80

<210> SEQ ID NO 103
<211> LENGTH: 56
<212> TYPE: PRT
<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 103

Met Val His His Val Arg Val Gln Val Pro His Arg Glu Phe Gly Asp
1 5 10 15

Val Ser Phe Ala Val Val Phe Asp Glu Asn Phe Thr Leu Asp Phe Cys
20 25 30

Ile His Met His Arg Thr Gly Val Pro Pro Thr Leu Ala Thr Gly Leu
35 40 45

Gly Phe Cys Ser Met Asn Arg Arg
50 55

<210> SEQ ID NO 104
<211> LENGTH: 68
<212> TYPE: PRT
<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 104

Met Glu Thr Ile Arg Leu Val Thr Ala Gly Lys Pro Tyr Lys Arg Phe
1 5 10 15

Glu Gln Ser Pro Phe Val Thr Met Ser Arg Ser Glu Tyr Glu Leu Arg
20 25 30

Thr Ala Pro Asn Ala Asn Asn Asp Tyr Ser Phe Val Met Arg Met Gly
35 40 45

Asn Lys Thr Arg Ile Val Asn Leu Trp Ala Pro Val His Gly Gln Val
50 55 60

Val Leu Tyr Asp
65

<210> SEQ ID NO 105
<211> LENGTH: 62
<212> TYPE: PRT
<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 105

Met Lys Val Gly Arg Ile Thr Ile Pro Ser Pro Ser Arg Arg Pro Arg
1 5 10 15

Trp Thr Thr Phe Tyr Phe Pro Ser Ser Arg Lys Thr Asp Arg Thr Arg
20 25 30

Leu Ala Glu Leu Ala Thr Phe Leu Val Gln Phe Ser Lys Leu Ser Val
35 40 45

Val Ala Pro Arg Ala Thr Met Leu Leu Val Arg Arg Thr Lys
50 55 60

<210> SEQ ID NO 106
<211> LENGTH: 6627
<212> TYPE: DNA
<213> ORGANISM: mosquito baculovirus
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (5397)...(6627)
<221> NAME/KEY: CDS
<222> LOCATION: (3517)...(4503)
<221> NAME/KEY: CDS
<222> LOCATION: (884)...(1588)

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<221> NAME/KEY: CDS
<222> LOCATION: (43)...(705)
<221> NAME/KEY: CDS
<222> LOCATION: (4818)...(5120)
<221> NAME/KEY: CDS
<222> LOCATION: (2029)...(2184)

<400> SEQUENCE: 106

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Leu Asp Pro Ile	
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gcg gtg gtc cca cta ccc tac att cac ggt gaa cat ttt cac aac tcg	102
Ala Val Val Pro Leu Pro Tyr Ile His Gly Glu His Phe His Asn Ser	
5 10 15 20	
tgg gac gtg atg cac ctc atg gcc gag gtg ggc gac caa att gtt gcc	150
Trp Asp Val Met His Leu Met Ala Glu Val Gly Asp Gln Ile Val Ala	
25 30 35	
caa cgt aat gac atg ttg gcg ctc gca cca ctg caa gtt gtg cac aac	198
Gln Arg Asn Asp Met Leu Ala Leu Ala Pro Leu Gln Val Val His Asn	
40 45 50	
gtg gtg gca aac atg tac att tcg ttg ggc tgc caa acc tgc gtt tca	246
Val Val Ala Asn Met Tyr Ile Ser Leu Gly Cys Gln Thr Cys Val Ser	
55 60 65	
cac tac cta ttg ttg cgg ggc gtc ata ctg gta aag ttc gaa caa ctc	294
His Tyr Leu Leu Leu Arg Gly Val Ile Leu Val Lys Phe Glu Gln Leu	
70 75 80	
ttc cgc cta ctg gtg ctc gag gag cta aag cgc cgt gaa ggt tcc att	342
Phe Arg Leu Leu Val Leu Glu Leu Lys Arg Arg Glu Gly Ser Ile	
85 90 95 100	
tcg ggc cgc acc atc gag ttg ctg cga atc cca acc gtt gag ctg gac	390
Ser Gly Arg Thr Ile Glu Leu Leu Arg Ile Pro Thr Val Glu Leu Asp	
105 110 115	
gag tac atc gcc aac ccc ggc gta ctg aac aac gcc ttt gtt aaa aat	438
Glu Tyr Ile Ala Asn Pro Gly Val Leu Asn Asn Ala Phe Val Lys Asn	
120 125 130	
tta cta gcg tac gaa atg gtc cag ctg cac aac tat atc aac tcg tac	486
Leu Leu Ala Tyr Glu Met Val Gln Leu His Asn Tyr Ile Asn Ser Tyr	
135 140 145	
cga att gta caa cag gcc agt gga cat ttg cgc agc aac aga ccc atc	534
Arg Ile Val Gln Gln Ala Ser Gly His Leu Arg Ser Asn Arg Pro Ile	
150 155 160	
gaa cag gcc gac atc aag gtc tac ctc aaa gcg ttc caa gaa ggc cca	582
Glu Gln Ala Asp Ile Lys Val Tyr Leu Lys Ala Phe Gln Glu Gly Pro	
165 170 175 180	
acc atg acc tgg gaa ctg tac gac aag cag agg cgc ggt gaa att gca	630
Thr Met Thr Trp Glu Leu Tyr Asp Lys Gln Arg Arg Gly Glu Ile Ala	
185 190 195	
ccc att tca ccc gta cga aag cga ccc gca ccg gat gat agc act ggt	678
Pro Ile Ser Pro Val Arg Lys Arg Pro Ala Pro Asp Asp Ser Thr Gly	
200 205 210	
cca ccg cta aag tat tcc agg gcc caa taaattacat tggactttt	725
Pro Pro Leu Lys Tyr Ser Arg Ala Gln	
215 220	
tttatata taattactat gggtagtgt gataacaacga taataaatat tggtaattt	785
caaccagaaa catttattta tttatctatt tattaatttt atatatttt atttcaaaaa	845
tatatacacgc tacactttcg ctactgtcga taccgcgg atg ttg tca ata atg ttt	901
Met Leu Ser Ile Met Phe	
225	
tcg cgc ttc ttc tca cgg aac att gac gca ccc tca cgg cgc tca acg	949
Ser Arg Phe Phe Ser Arg Asn Ile Asp Ala Pro Ser Arg Arg Ser Thr	

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230	235	240	
atg ttt atg gcg gag cggt tac gga ttc ttt atc gat cgt ctg gac Met Phe Met Ala Glu Arg Val Tyr Gly Phe Phe Ile Asp Arg Leu Asp 245 250 255			997
att cgt tcg tac ttc tcg agg gca tcc ttt tgc gct acc aaa tcg tta Ile Arg Ser Tyr Phe Ser Arg Ala Ser Phe Cys Ala Thr Lys Ser Leu 260 265 270 275			1045
tac tcg gac agg gcc aaa atg tcg tac tgt ggt tcc aat atg acg gtg Tyr Ser Asp Arg Ala Lys Met Ser Tyr Cys Gly Ser Asn Met Thr Val 280 285 290			1093
cga tcg atc aac ttg tcg cgc aac ttg ggg tcc atc gaa aga aag ttt Arg Ser Ile Asn Leu Ser Arg Asn Leu Gly Ser Ile Glu Arg Lys Phe 295 300 305			1141
tca gac ttg gac agc aaa cga ccc tgg ttc agt ttg cgc aat ctt cgc Ser Asp Leu Asp Ser Lys Arg Pro Trp Phe Ser Leu Arg Asn Leu Arg 310 315 320			1189
gtt tgg ctc ttg agc tcc att tcc tcc cgc ttc agc tgc tcc atg cgc Val Trp Leu Leu Ser Ser Ile Ser Arg Phe Ser Cys Ser Met Arg 325 330 335			1237
tca cgt ttc gcc gca tca cgc tca ctc acc gca gag tac agc aac ttg Ser Arg Phe Ala Ala Ser Arg Ser Leu Thr Ala Glu Tyr Ser Asn Leu 340 345 350 355			1285
tta tcc tcc agc agc ctg gac aac ctt tca tcg tca atc acc tgc ttc Leu Ser Ser Ser Leu Asp Asn Leu Ser Ser Ser Ile Thr Cys Phe 360 365 370			1333
gat tta aac cca aac agc ttg cgc tct tca tcc gtg tac ttg ccc cca Asp Leu Asn Pro Asn Ser Leu Arg Ser Ser Ser Val Tyr Leu Pro Pro 375 380 385			1381
caa tcc gct tta gct tca ctc gtg gca ccg tca acc tta tcc gtt tca Gln Ser Ala Leu Ala Ser Leu Val Ala Pro Ser Thr Leu Ser Val Ser 390 395 400			1429
ccg cac agg aaa cgc gtc agc tcc ttc aat aac ctg att ttg tac cgg Pro His Arg Lys Arg Val Ser Ser Phe Asn Asn Leu Ile Leu Tyr Arg 405 410 415			1477
tca tat tcg acc ggg acg tgc ttt cca tcg acg gga acc tca gaa tat Ser Tyr Ser Thr Gly Thr Cys Phe Pro Ser Thr Gly Thr Ser Glu Tyr 420 425 430 435			1525
acc tcg tgg atc aag gtg aac gtt acg tcg cag ccc atc ttt aat cgg Thr Ser Trp Ile Lys Val Asn Val Thr Ser Gln Pro Ile Phe Asn Arg 440 445 450			1573
tgt caa ctt aaa ctc tagacaccct gtacgtcttt cgtacggcgt tgagtacggt Cys Gln Leu Lys Leu 455			1628
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cgcctgctct tcaatttagta tacggcggt gaggcagcggt tcaccgtact gtgcttccgc			1748
aatatgtaac aatttatcca cctttcaga cagcgcatgg ttcacggcgt acagggccaa			1808
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cagtgggata caatggatca accgttgtga cattagaaac aaacgcttct cgaccgcagt			1928
catcgtctca ttgtccaccc tatccaccag tcgtgc当地 aacgttcataa ttttcgcataa			1988
gaagaaggtg ggcttgcgt tgcaggat ttgtggcaca atg ttt tcg ttg aaa Met Phe Ser Leu Lys 460			2043
tct ttg aaa att ttt gcc ata ttc agc tgc tcc aag cac ccc tcg gcc Ser Leu Lys Ile Phe Ala Ile Phe Ser Cys Ser Lys His Pro Ser Ala 465 470 475			2091
aac tgg agc gtg ttg gcc tgg tcc aca ccg cgg ctc agg ttg ttg agg			2139

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Asn Trp Ser Val Leu Ala Trp Ser Thr Pro Arg Leu Arg Leu Leu Arg			
480	485	490	
gca att gaa tac ggc acg gtt tcc cga tac tgg gtc agg tcc aca	2184		
Ala Ile Glu Tyr Gly Thr Val Ser Arg Tyr Trp Val Arg Ser Thr			
495	500	505	
tagtcgtgca ccttcgagtc gtgcggta ccttcggcga ttatgttagt tttcgtgcgg	2244		
aacgagagca gctctccaa ccttggta taattgtcca gtatgtgtag cacaacctgg	2304		
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gcggcccttt tcaagtcctg tgccatgaaa tcgcgcacta ggtccgtaat aatgtcgttt	2484		
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agactttctc gccgaaagg gttataatca atccggagac gaaggagattt gaagttcg	3504		
cagtttgcag tg atg gag ttg gat aca ctt act tca cgg tcg gtc aaa tgc	3555		
Met Glu Leu Asp Thr Leu Thr Ser Arg Ser Val Lys Cys			
510	515	520	
ctc acc ctg tta ccg aac gtg acg tta gcg gcg gtt cat cga aca aaa	3603		
Leu Thr Leu Leu Pro Asn Val Thr Leu Ala Ala Val His Arg Thr Lys			
525	530	535	
tcc caa gcc ggt cgc gag ggt cgg cgg aac ccc tgt ccg gtg cat gtg	3651		
Ser Gln Ala Gly Arg Glu Gly Arg Arg Asn Pro Cys Pro Val His Val			
540	545	550	
gat aca aaa atc aag tgg aaa att ttc atc aaa aac tac agc aaa act	3699		
Asp Thr Lys Ile Lys Cys Lys Ile Phe Ile Lys Asn Tyr Ser Lys Thr			
555	560	565	
cac gtc acc gaa ctc tcg atg ggg tac ctg aac tcg aac atg gtg cac	3747		
His Val Thr Glu Leu Ser Met Gly Tyr Leu Asn Ser Asn Met Val His			
570	575	580	585
cat tat gtg gcc ctg atg ggc atg tgc agg gaa aac cga ggt aca gtt	3795		
His Tyr Val Ala Leu Met Gly Met Cys Arg Glu Asn Arg Gly Thr Val			
590	595	600	
gac gcc tgt tta tac gcg tcc aac aag atc aat tgg gtg ctg cgg ttc	3843		
Asp Ala Cys Leu Tyr Ala Ser Asn Lys Ile Asn Cys Val Leu Arg Phe			
605	610	615	

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gac ctg gac ctg ttc cgc tcc agc ttt ggg ggt aga gtt ata aac att Asp Leu Asp Leu Phe Arg Ser Ser Phe Gly Gly Arg Val Ile Asn Ile 620 625 630	3891
ggc cac gtt tac gat gaa ctt gac cgc ata tac aga acg cta gat aga Gly His Val Tyr Asp Glu Leu Asp Arg Ile Tyr Arg Thr Leu Asp Arg 635 640 645	3939
caa att tta att tcg ccc aac tcg gcg cta gag ttg tac gtt agc gcg Gln Ile Leu Ile Ser Pro Asn Ser Ala Leu Glu Leu Tyr Val Ser Ala 650 655 660 665	3987
gaa tct gct gtg cta gca cca cag gac ctc ctc att ata cac ccc ttc Glu Ser Ala Val Ala Pro Gln Asp Leu Leu Ile His Pro Phe 670 675 680	4035
gtt gaa gat ctc gag tac cca ctg gtc tcg cgc ggc tac cca ctg gac Val Glu Asp Leu Glu Tyr Pro Leu Val Ser Arg Gly Tyr Pro Leu Asp 685 690 695	4083
gac gag gtg ata gta aat tac cgc tac tac agg gcc gtg ttg att gcc Asp Glu Val Ile Val Asn Tyr Arg Tyr Arg Ala Val Leu Ile Ala 700 705 710	4131
atc acg ctc gta acc tgc ctg att ggt aac agc gat ttg ctc agc aca Ile Thr Leu Val Thr Cys Leu Ile Gly Asn Ser Asp Leu Leu Ser Thr 715 720 725	4179
acc atg gcc gca tcg aaa atc atc cac agc gtt ggc att tgc ccg tac Thr Met Ala Ala Ser Lys Ile Ile His Ser Val Gly Ile Cys Pro Tyr 730 735 740 745	4227
tac ccg gac cat atg gcg gtc tgt aaa ctg acg aac cgc gtt acg ggg Tyr Pro Asp His Met Ala Val Cys Lys Leu Thr Asn Arg Val Thr Gly 750 755 760	4275
acg gtc atg gat agg cac atc ttc tgc atc cca atc gag cag ttc aaa Thr Val Met Asp Arg His Ile Phe Cys Ile Pro Ile Glu Gln Phe Lys 765 770 775	4323
cgg tcc ttt cta tac cgc aaa acc gtt atc aag cgg gac ggt gag gat Arg Ser Phe Leu Tyr Arg Lys Thr Val Ile Lys Arg Asp Gly Glu Asp 780 785 790	4371
aag gcg gtg gac att aag tcg tta aaa tct atg acc cag aat ata cgc Lys Ala Val Asp Ile Lys Ser Leu Lys Ser Met Thr Gln Asn Ile Arg 795 800 805	4419
gga aag cgc aac ccc agt ccc gag ttg tgg aac gtt ttt acg aag aac Gly Lys Arg Asn Pro Ser Pro Glu Leu Trp Asn Val Phe Thr Lys Asn 810 815 820 825	4467
atc gag gaa ctt ttt gtt cga tac gac aat gca gtt tgagatttag Ile Glu Glu Leu Phe Val Arg Tyr Asp Asn Ala Val 830 835	4513
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accacattcg gcgcgggtga acatattgcc gaggtgaact ttatcaaacc taaaggctgt	4813
ggag atg gaa aac gtt cgg tcg aca cca ccg tcg ttg aac caa acg aac Met Glu Asn Val Arg Ser Thr Pro Pro Ser Leu Asn Gln Thr Asn 840 845 850	4862
cgg tta aca agc gcg ccc gta cgc cga gtc cag ccc cag tcg atc aag Arg Leu Thr Ser Ala Pro Val Arg Arg Val Gln Pro Gln Ser Ile Lys 855 860 865	4910
att tgc ccg aac caa aac cag agc ccg agt ctg cag ctg aac cgg gac Ile Cys Pro Asn Gln Asn Ser Pro Ser Leu Gln Leu Asn Arg Asp 870 875 880	4958
cag agc tgc ccg ata tgc caa ctg atg atg ccc aac tcg agc acg agc	5006

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Gln Ser Cys Pro Ile Cys Gln Leu Met Met	Pro Asn Ser Ser Thr Ser	
885 890	895	900
ccg agc ccg atc caa agc ccg agc ctg agc ctg agt ccg act cta gag		5054
Pro Ser Pro Ile Gln Ser Pro Ser Leu Ser Leu Ser Pro Thr Leu Glu		
905 910		915
aac cag tgc cag cag cac cag tcg tcg ctc cgg ttg atg gac atg ttg		5102
Asn Gln Cys Gln Gln His Gln Ser Ser Leu Arg Leu Met Asp Met Leu		
920 925		930
atg agt cgc cgc agt tgg tagaaggta gtttgaaggt agaaaataata		5150
Met Ser Arg Arg Ser Trp		
935		
aaaatatttt ccccccaaac ccagattcgt tttttttttt aatgcatac acagcaaatt		5210
accgatgatc agaccggccc cgaattgggc cacttgaaa cataggttgt gaggtggta		5270
ggtggactct agctacaacgg tccattttat aataaaaatta atatcatttt ttttattaaac		5330
ctaaaagttt cggtttatgc gctataaaag ggtggagctg tcccgatgtgg tgccgatagt		5390
gaagtc atg gcg tgc aac gat cta gag ctc aag ttc caa gtg tgg acc		5438
Met Ala Cys Asn Asp Leu Glu Leu Lys Phe Gln Val Trp Thr		
940 945		950
gtg gtg gga tac ggt ggt gct gag ctt gtg tta caa ttt tac cac ttt		5486
Val Val Gly Tyr Gly Gly Ala Glu Leu Val Leu Gln Phe Tyr His Phe		
955 960		965
acc gaa cca acc agt gga aag gtt tac gtt tct ggg cgc acc gtc agc		5534
Thr Glu Pro Thr Ser Gly Lys Val Tyr Val Ser Gly Arg Thr Val Ser		
970 975		980
gcg ggc ctc ggc ttc aag gat ccc acg gcc agc atg tgc cgc aag gtt		5582
Ala Gly Leu Gly Phe Lys Asp Pro Thr Ala Ser Met Cys Arg Lys Val		
985 990		995 1000
tcc agc cga aat cgc atc cag tgg aag gtt ttg ggc ggg ttg tgc		5630
Ser Ser Arg Asn Arg Ile Gln Trp Lys Val Leu Ala Ala Gly Leu Cys		
1005 1010		1015
gta aaa ttg ccc atc aat tgg aag atg gaa acg acg atg ata aat cga		5678
Val Lys Leu Pro Ile Asn Trp Lys Met Glu Thr Thr Met Ile Asn Arg		
1020 1025		1030
gat gga ctg cgc caa ctg gcg gcc acc aag gag ggt att tgg ccc cag		5726
Asp Gly Leu Arg Gln Leu Ala Ala Thr Lys Glu Gly Ile Trp Pro Gln		
1035 1040		1045
cta agc aaa ctg tgg aac gaa acg ttt gac tgt aac ttt ttc gaa gac		5774
Leu Ser Lys Leu Trp Asn Glu Thr Phe Asp Cys Asn Phe Phe Glu Asp		
1050 1055		1060
gat aat att atc gag gtt gac gat gtt ggg tcg agc gtt ttt cag		5822
Asp Asn Ile Ile Glu Val Glu Cys Asp Val Gly Ser Ser Val Phe Gln		
1065 1070		1075 1080
ctg caa aat tgg gac gtt gac gac aag agt gtc gtt ctg cgg ttg tac		5870
Leu Gln Asn Trp Asp Val Asp Asp Lys Ser Val Val Leu Arg Leu Tyr		
1085 1090		1095
atc cac ccg atc acc aac gag ccg tgg gtc gtt ggc gcg gat cta gcg		5918
Ile His Pro Ile Thr Asn Glu Pro Trp Val Val Ala Ala Asp Leu Ala		
1100 1105		1110
cgc tgc ttg ggt tac gaa aag tat cgc caa acg cac acg cga atc ctc		5966
Arg Cys Leu Gly Tyr Glu Lys Tyr Arg Gln Thr His Thr Arg Ile Leu		
1115 1120		1125
gcc gcc ttc aag cga aag ctg tcg gac cta gtt cac acc gaa cct ttt		6014
Ala Ala Phe Lys Arg Lys Leu Ser Asp Leu Val His Thr Glu Pro Phe		
1130 1135		1140
tcg ggt acc gtt gaa tca gag gta gca cga ctg gag ggt gca ccg gtg		6062
Ser Gly Thr Val Glu Ser Glu Val Ala Arg Leu Glu Gly Ala Pro Val		
1145 1150		1155 1160

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gag cta tcg tct cgc gaa cgg gac att gtg gtg gtc aac gag ggt gga Glu Leu Ser Ser Arg Glu Arg Asp Ile Val Val Val Asn Glu Gly Gly 1165 1170 1175	6110
atc cac cag atg ctg atc ggt tca cgg ctg ccc aat gtg caa aag tac Ile His Gln Met Leu Ile Gly Ser Arg Leu Pro Asn Val Gln Lys Tyr 1180 1185 1190	6158
aag gag ctt gtg ttt ggt aaa att tta cca cgg gcc cgt gcc cga ggt Lys Glu Leu Val Phe Gly Lys Ile Leu Pro Ala Ala Arg Ala Arg Gly 1195 1200 1205	6206
gag ctg caa att ggc acc att gga cag ggt gat gga ggt gca gtg gag Glu Leu Gln Ile Gly Thr Ile Gly Gln Gly Asp Gly Ala Val Glu 1210 1215 1220	6254
ccc aca aat caa cta cag tca aac gaa aag att ttg gag ctg gag ttg Pro Thr Asn Gln Leu Gln Ser Asn Glu Lys Ile Leu Glu Leu Glu Leu 1225 1230 1235 1240	6302
gcc ctg tcg cgg tcc aat agt gaa ttg aaa gtg gtc aag ttg gaa cag Ala Leu Ser Arg Ser Asn Ser Glu Leu Lys Val Val Lys Leu Glu Gln 1245 1250 1255	6350
ttg cgc gta cag gaa tcg tac gag tct aaa ttg aaa att acc gat atg Leu Arg Val Gln Glu Ser Tyr Glu Ser Lys Leu Lys Ile Thr Asp Met 1260 1265 1270	6398
gag cac cgg cgc atg aag ctc gag tgc aag ctg aag ctg atc gag ctg Glu His Arg Arg Met Lys Leu Glu Cys Lys Leu Lys Leu Ile Glu Leu 1275 1280 1285	6446
gca atg ggt atc ggt aaa cgg gac cag ttg atc gcc gac acg tac cgc Ala Met Gly Ile Gly Lys Arg Asp Gln Leu Ile Ala Asp Thr Tyr Arg 1290 1295 1300	6494
gat att cag gaa att tgt gaa ggc ctc tca ccg cac att gtc ccc gag Asp Ile Gln Glu Ile Cys Glu Gly Leu Ser Pro His Ile Val Pro Glu 1305 1310 1315 1320	6542
gtg ccc agc tgc aag ctg aac tat atc gca ctg tac gaa cgt gca gtt Val Pro Ser Cys Lys Leu Asn Tyr Ile Ala Leu Tyr Glu Arg Ala Val 1325 1330 1335	6590
gga gag ggc aaa cgg gtg gtg cga gtg tgc aga att c Gly Glu Gly Lys Arg Val Val Arg Val Cys Arg Ile 1340 1345	6627

<210> SEQ ID NO 107
<211> LENGTH: 221
<212> TYPE: PRT
<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 107

Leu Asp Pro Ile Ala Val Val Pro Tyr Ile His Gly Glu His 1 5 10 15
Phe His Asn Ser Trp Asp Val Met His Leu Met Ala Glu Val Gly Asp 20 25 30
Gln Ile Val Ala Gln Arg Asn Asp Met Leu Ala Leu Ala Pro Leu Gln 35 40 45
Val Val His Asn Val Val Ala Asn Met Tyr Ile Ser Leu Gly Cys Gln 50 55 60
Thr Cys Val Ser His Tyr Leu Leu Leu Arg Gly Val Ile Leu Val Lys 65 70 75 80
Phe Glu Gln Leu Phe Arg Leu Leu Val Leu Glu Glu Leu Lys Arg Arg 85 90 95
Glu Gly Ser Ile Ser Gly Arg Thr Ile Glu Leu Leu Arg Ile Pro Thr 100 105 110
Val Glu Leu Asp Glu Tyr Ile Ala Asn Pro Gly Val Leu Asn Asn Ala 115 120 125

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Phe Val Lys Asn Leu Leu Ala Tyr Glu Met Val Gln Leu His Asn Tyr
130           135           140

Ile Asn Ser Tyr Arg Ile Val Gln Gln Ala Ser Gly His Leu Arg Ser
145           150           155           160

Asn Arg Pro Ile Glu Gln Ala Asp Ile Lys Val Tyr Leu Lys Ala Phe
165           170           175

Gln Glu Gly Pro Thr Met Thr Trp Glu Leu Tyr Asp Lys Gln Arg Arg
180           185           190

Gly Glu Ile Ala Pro Ile Ser Pro Val Arg Lys Arg Pro Ala Pro Asp
195           200           205

Asp Ser Thr Gly Pro Pro Leu Lys Tyr Ser Arg Ala Gln
210           215           220

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<210> SEQ ID NO 108
<211> LENGTH: 235
<212> TYPE: PRT
<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 108

Met Leu Ser Ile Met Phe Ser Arg Phe Phe Ser Arg Asn Ile Asp Ala
1           5           10           15

Pro Ser Arg Arg Ser Thr Met Phe Met Ala Glu Arg Val Tyr Gly Phe
20          25          30

Phe Ile Asp Arg Leu Asp Ile Arg Ser Tyr Phe Ser Arg Ala Ser Phe
35          40          45

Cys Ala Thr Lys Ser Leu Tyr Ser Asp Arg Ala Lys Met Ser Tyr Cys
50          55          60

Gly Ser Asn Met Thr Val Arg Ser Ile Asn Leu Ser Arg Asn Leu Gly
65          70          75          80

Ser Ile Glu Arg Lys Phe Ser Asp Leu Asp Ser Lys Arg Pro Trp Phe
85          90          95

Ser Leu Arg Asn Leu Arg Val Trp Leu Leu Ser Ser Ile Ser Ser Arg
100         105         110

Phe Ser Cys Ser Met Arg Ser Arg Phe Ala Ala Ser Arg Ser Leu Thr
115         120         125

Ala Glu Tyr Ser Asn Leu Leu Ser Ser Ser Leu Asp Asn Leu Ser
130         135         140

Ser Ser Ile Thr Cys Phe Asp Leu Asn Pro Asn Ser Leu Arg Ser Ser
145         150         155         160

Ser Val Tyr Leu Pro Pro Gln Ser Ala Leu Ala Ser Leu Val Ala Pro
165         170         175

Ser Thr Leu Ser Val Ser Pro His Arg Lys Arg Val Ser Ser Phe Asn
180         185         190

Asn Leu Ile Leu Tyr Arg Ser Tyr Ser Thr Gly Thr Cys Phe Pro Ser
195         200         205

Thr Gly Thr Ser Glu Tyr Thr Ser Trp Ile Lys Val Asn Val Thr Ser
210         215         220

Gln Pro Ile Phe Asn Arg Cys Gln Leu Lys Leu
225         230         235

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<210> SEQ ID NO 109
<211> LENGTH: 52
<212> TYPE: PRT
<213> ORGANISM: mosquito baculovirus

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<400> SEQUENCE: 109

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Met Phe Ser Leu Lys Ser Leu Lys Ile Phe Ala Ile Phe Ser Cys Ser
 1           5          10          15

Lys His Pro Ser Ala Asn Trp Ser Val Leu Ala Trp Ser Thr Pro Arg
 20          25          30

Leu Arg Leu Leu Arg Ala Ile Glu Tyr Gly Thr Val Ser Arg Tyr Trp
 35          40          45

Val Arg Ser Thr
 50

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<210> SEQ_ID NO 110
<211> LENGTH: 329
<212> TYPE: PRT
<213> ORGANISM: mosquito baculovirus

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<400> SEQUENCE: 110

Met Glu Leu Asp Thr Leu Thr Ser Arg Ser Val Lys Cys Leu Thr Leu
 1           5          10          15

Leu Pro Asn Val Thr Leu Ala Ala Val His Arg Thr Lys Ser Gln Ala
 20          25          30

Gly Arg Glu Gly Arg Arg Asn Pro Cys Pro Val His Val Asp Thr Lys
 35          40          45

Ile Lys Cys Lys Ile Phe Ile Lys Asn Tyr Ser Lys Thr His Val Thr
 50          55          60

Glu Leu Ser Met Gly Tyr Leu Asn Ser Asn Met Val His His Tyr Val
 65          70          75          80

Ala Leu Met Gly Met Cys Arg Glu Asn Arg Gly Thr Val Asp Ala Cys
 85          90          95

Leu Tyr Ala Ser Asn Lys Ile Asn Cys Val Leu Arg Phe Asp Leu Asp
100         105         110

Leu Phe Arg Ser Ser Phe Gly Gly Arg Val Ile Asn Ile Gly His Val
115         120         125

Tyr Asp Glu Leu Asp Arg Ile Tyr Arg Thr Leu Asp Arg Gln Ile Leu
130         135         140

Ile Ser Pro Asn Ser Ala Leu Glu Leu Tyr Val Ser Ala Glu Ser Ala
145         150         155         160

Val Leu Ala Pro Gln Asp Leu Leu Ile Ile His Pro Phe Val Glu Asp
165         170         175

Leu Glu Tyr Pro Leu Val Ser Arg Gly Tyr Pro Leu Asp Asp Glu Val
180         185         190

Ile Val Asn Tyr Arg Tyr Tyr Arg Ala Val Leu Ile Ala Ile Thr Leu
195         200         205

Val Thr Cys Leu Ile Gly Asn Ser Asp Leu Leu Ser Thr Thr Met Ala
210         215         220

Ala Ser Lys Ile Ile His Ser Val Gly Ile Cys Pro Tyr Tyr Pro Asp
225         230         235         240

His Met Ala Val Cys Lys Leu Thr Asn Arg Val Thr Gly Thr Val Met
245         250         255

Asp Arg His Ile Phe Cys Ile Pro Ile Glu Gln Phe Lys Arg Ser Phe
260         265         270

Leu Tyr Arg Lys Thr Val Ile Lys Arg Asp Gly Glu Asp Lys Ala Val
275         280         285

Asp Ile Lys Ser Leu Lys Ser Met Thr Gln Asn Ile Arg Gly Lys Arg
290         295         300

Asn Pro Ser Pro Glu Leu Trp Asn Val Phe Thr Lys Asn Ile Glu Glu

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305	310	315	320
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Leu Phe Val Arg Tyr Asp Asn Ala Val
325

<210> SEQ_ID NO 111
<211> LENGTH: 101
<212> TYPE: PRT
<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 111

Met Glu Asn Val Arg Ser Thr Pro Pro Ser	Leu Asn Gln Thr Asn Arg		
1	5	10	15

Leu Thr Ser Ala Pro Val Arg Arg Val Gln Pro Gln Ser	Ile Lys Ile		
20	25	30	

Cys Pro Asn Gln Asn Gln Ser Pro Ser	Leu Gln Leu Asn Arg Asp Gln		
35	40	45	

Ser Cys Pro Ile Cys Gln Leu Met Met Pro Asn Ser	Ser Thr Ser Pro		
50	55	60	

Ser Pro Ile Gln Ser Pro Ser	Leu Ser Pro	Thr Leu Glu Asn	
65	70	75	80

Gln Cys Gln Gln His Gln Ser Ser	Leu Arg Leu Met Asp Met	Leu Met	
85	90	95	

Ser Arg Arg Ser Trp			
100			

<210> SEQ_ID NO 112
<211> LENGTH: 410
<212> TYPE: PRT
<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 112

Met Ala Cys Asn Asp Leu Glu Leu Lys Phe Gln Val Trp Thr Val Val			
1	5	10	15

Gly Tyr Gly Gly Ala Glu Leu Val Leu Gln Phe Tyr His Phe Thr Glu			
20	25	30	

Pro Thr Ser Gly Lys Val Tyr Val Ser Gly Arg Thr Val Ser Ala Gly			
35	40	45	

Leu Gly Phe Lys Asp Pro Thr Ala Ser Met Cys Arg Lys Val Ser Ser			
50	55	60	

Arg Asn Arg Ile Gln Trp Lys Val Leu Ala Ala Gly Leu Cys Val Lys			
65	70	75	80

Leu Pro Ile Asn Trp Lys Met Glu Thr Thr Met Ile Asn Arg Asp Gly			
85	90	95	

Leu Arg Gln Leu Ala Ala Thr Lys Glu Gly Ile Trp Pro Gln Leu Ser			
100	105	110	

Lys Leu Trp Asn Glu Thr Phe Asp Cys Asn Phe Phe Glu Asp Asp Asn			
115	120	125	

Ile Ile Glu Val Glu Cys Asp Val Gly Ser Ser Val Phe Gln Leu Gln			
130	135	140	

Asn Trp Asp Val Asp Asp Lys Ser Val Val Leu Arg Leu Tyr Ile His			
145	150	155	160

Pro Ile Thr Asn Glu Pro Trp Val Val Ala Ala Asp Leu Ala Arg Cys			
165	170	175	

Leu Gly Tyr Glu Lys Tyr Arg Gln Thr His Thr Arg Ile Leu Ala Ala			
180	185	190	

Phe Lys Arg Lys Leu Ser Asp Leu Val His Thr Glu Pro Phe Ser Gly

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195	200	205
Thr Val Glu Ser Glu Val Ala Arg Leu Glu Gly Ala Pro Val Glu Leu		
210	215	220
Ser Ser Arg Glu Arg Asp Ile Val Val Asn Glu Gly Gly Ile His		
225	230	235
Gln Met Leu Ile Gly Ser Arg Leu Pro Asn Val Gln Lys Tyr Lys Glu		
245	250	255
Leu Val Phe Gly Lys Ile Leu Pro Ala Ala Arg Ala Arg Gly Glu Leu		
260	265	270
Gln Ile Gly Thr Ile Gly Gln Gly Asp Gly Gly Ala Val Glu Pro Thr		
275	280	285
Asn Gln Leu Gln Ser Asn Glu Lys Ile Leu Glu Leu Glu Leu Ala Leu		
290	295	300
Ser Arg Ser Asn Ser Glu Leu Lys Val Val Lys Leu Glu Gln Leu Arg		
305	310	315
Val Gln Glu Ser Tyr Glu Ser Lys Leu Lys Ile Thr Asp Met Glu His		
325	330	335
Arg Arg Met Lys Leu Glu Cys Lys Leu Lys Leu Ile Glu Leu Ala Met		
340	345	350
Gly Ile Gly Lys Arg Asp Gln Leu Ile Ala Asp Thr Tyr Arg Asp Ile		
355	360	365
Gln Glu Ile Cys Glu Gly Leu Ser Pro His Ile Val Pro Glu Val Pro		
370	375	380
Ser Cys Lys Leu Asn Tyr Ile Ala Leu Tyr Glu Arg Ala Val Gly Glu		
385	390	395
Gly Lys Arg Val Val Arg Val Cys Arg Ile		
405	410	

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<210> SEQ_ID NO 113
<211> LENGTH: 6627
<212> TYPE: DNA
<213> ORGANISM: mosquito baculovirus
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (4481)....(5128)
<221> NAME/KEY: CDS
<222> LOCATION: (3240)....(3668)
<221> NAME/KEY: CDS
<222> LOCATION: (6145)....(6327)

<400> SEQUENCE: 113

gaattcgtt cccactacaa cagcgccgccc aaggagtgcg agctggaccc cattgcggtg      60
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atggccgagg tggcgacca aatttgtgcc caacgtaatg acatgttggc gctcgaccca     180
ctgcaagttg tgcacaacgt ggtggcaaac atgtacattt cgttgggctg ccaaacctgc     240
gtttcacact acctattgtt gcggggcgtc atactggtaa agttcgaaca actcttccgc     300
ctactggtgc tcgaggagct aaagcgcgt gaaggttcca ttccggccg caccatcgag     360
ttgctgcga tcccaaccgt tgagctggac ggtacatcg ccaaccccg cgtactgaac     420
aacgcctttg ttaaaaattt actagcgtac gaaatggtcc agctgcacaa ctatataac     480
tcgtaccgaa ttgtacaaca ggcagtgga catttgcgc gcaacagacc catcgaacag     540
gccgacatca aggtctacct caaagcgttc caagaaggcc caaccatgac ctggaaactg     600
tacgacaagc agaggcgcgg tgaaattgca cccatttcac ccgtacgaaa gcgacccgca     660
ccggatgata gcactggtcc accgctaaag tattccaggg cccaataaaat tacattggac     720

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aatttcaacc agaaaacattt atttattttt ctatttatta attttataa tttatatttc	840
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tgcgcgttc ttctcacgga acattgacgc accctcacgg cgctcaacga tggttatggc	960
ggagcgggtg tacggattct ttatcgatcg tctggacatt cggtcgact tctcgaggc	1020
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caatatgacg gtgcgatcga tcaacttgac gcgcaacttg gggtccatcg aaagaaaatt	1140
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gagctccatt tcctcccgct tcagctgctc catgcgcgtca cgtttcgcgc catcacgctc	1260
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ctg gcc gtg tac ggg cgc cca gag gtt cac aat acg tgt ctt att acc Leu Ala Val Tyr Gly Arg Pro Glu Val His Asn Thr Cys Leu Ile Thr	3287
1 5 10 15	
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20 25 30	
cag ttc gta ttc aga gca gtc att gtt aac aaa cgg cga ctg ctc aaa Gln Phe Val Phe Arg Ala Gly His Cys Asn Lys Arg Arg Leu Leu Lys	3383
35 40 45	
ccg ctt gta agg ttt acc ggc cgt aac gag gcg aat tgt ttc cat atg Pro Leu Val Arg Phe Thr Gly Arg Asn Glu Ala Asn Cys Phe His Met	3431
50 55 60	
gat gcg ttt acc gag act ttt ctg cgg caa agg gtt ata atc aat ccg Asp Ala Phe Thr Glu Thr Phe Leu Arg Gln Arg Val Ile Ile Asn Pro	3479
65 70 75 80	
gag acg aag gag att gaa gtt cgc gca gtt tgc agt gat gga gtt gga Glu Thr Lys Glu Ile Glu Val Arg Ala Val Cys Ser Asp Gly Val Gly	3527
85 90 95	
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100 105 110	
gac gtt acg ggc ggt tca tcg aac aaa atc cca acg cgg tcg cga ggg Asp Val Ser Gly Gly Ser Ser Asn Lys Ile Pro Ser Arg Ser Arg Gly	3623
115 120 125	
tcg gcg gaa ccc ctg tcc ggt gca tgt gga tac aaa aat caa gtg Ser Ala Glu Pro Leu Ser Gly Ala Cys Gly Tyr Lys Asn Gln Val	3668
130 135 140	
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gaacgtttt acgaagaaca tcgaggaact tt ttg ttc gat acg aca atg cag Leu Phe Asp Thr Thr Met Gln	4328
145 150	
ttt gag att gag atc acg aac ggt aac cag ttg tac tca tcg cgc aac Phe Glu Ile Glu Ile Ser Asn Gly Asn Gln Leu Tyr Ser Ser Arg Asn	4388
155 160 165	
caa cta att tta ccc ggg ctc acc gac gtg tac tat cac tat gta agc Gln Leu Ile Leu Pro Gly Leu Thr Asp Val Tyr Tyr His Tyr Val Ser	4448
170 175 180	

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cgc gag ggc acg gag ctc aat aag atc gct ttt cgt ctg caa gtg tac Arg Glu Gly Thr Glu Leu Asn Lys Ile Ala Phe Arg Leu Gln Val Tyr 215 220 225 230	4741
gtc ctt aaa gcg acc aca ttc ggc gcc ggt gaa cat att gcc gag gtg Val Leu Lys Ala Thr Thr Phe Gly Ala Gly Glu His Ile Ala Glu Val 235 240 245	4789
aac ttt atc aaa cct aaa ggc tgt gga gat gga aaa cgt tcg gtc gac Asn Phe Ile Lys Pro Lys Gly Cys Gly Asp Gly Lys Arg Ser Val Asp 250 255 260	4837
acc acc gtc gtt gaa cca aac gaa ccg gtt aac aag cgc gcc cgt acg Thr Thr Val Val Glu Pro Asn Glu Pro Val Asn Lys Arg Ala Arg Thr 265 270 275	4885
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ccc gag tct gca gct gaa ccg gga cca gag ctg ccc gat atg cca act Pro Glu Ser Ala Ala Glu Pro Gly Pro Glu Leu Pro Asp Met Pro Thr 295 300 305 310	4981
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gtt tagtttgaag gtagaaataa taaaaatatt ttcccccaa acccagattc Val	5178
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gccacttgga aacatagggt gtgaggttgt gaggtggact ctagctaac ggtccatttt	5298
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gtaccgttga atcagaggtt gcacgactgg agggtgccacc ggtggagcta tcgtctcgcg	6078
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tgccca atg tgc aaa agt aca agg agc ttg tgt ttg gta aaa ttt tac Met Cys Lys Ser Thr Arg Ser Leu Cys Leu Val Lys Phe Tyr 360 365 370	6186
cag cgg ccc gtg ccc gag gtg agc tgc aaa ttg gca cca ttg gac agg Gln Arg Pro Val Pro Glu Val Ser Cys Lys Leu Ala Pro Leu Asp Arg 375 380 385	6234
gtg atg gag gtg cag tgg agc cca caa atc aac tac agt caa acg aaa Val Met Glu Val Gln Trp Ser Pro Gln Ile Asn Tyr Ser Gln Thr Lys 390 395 400 405	6282
aga ttt tgg agc tgg agt tgg ccc tgt cgc ggt cca ata gtg aat Arg Phe Trp Ser Trp Ser Trp Pro Cys Arg Gly Pro Ile Val Asn 410 415 420	6327
tgaaagtgg caagttggaa cagttgcgc tacaggaatc gtacgagtct aaattgaaaa ttaccgatat ggagcacccg cgcataaaggc tcgactgcaa gctgaagctg atcgagctgg caatgggtat cggttaaacgg gaccagttga tcgcccacac gtaccgcgtat attcaggaaa tttgtgaagg cctctccaccg cacattgtcc ccgaggtgcc cagctgcaag ctgaactata tcgcactgta cgaacgtgca gttggagagg gcaaacgggt ggtgcgagtg tgcagaattc	6387 6447 6507 6567 6627

<210> SEQ ID NO 114

<211> LENGTH: 143

<212> TYPE: PRT

<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 114

Leu Ala Val Tyr Gly Arg Pro Glu Val His Asn Thr Cys Leu Ile Thr 1 5 10 15
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His Ser His His Glu Arg Val Val Ile Val Cys Val Arg Cys Gly Ser 20 25 30

Gln Phe Val Phe Arg Ala Gly His Cys Asn Lys Arg Arg Leu Leu Lys 35 40 45

Pro Leu Val Arg Phe Thr Gly Arg Asn Glu Ala Asn Cys Phe His Met 50 55 60

Asp Ala Phe Thr Glu Thr Phe Leu Arg Gln Arg Val Ile Ile Asn Pro 65 70 75 80
--

Glu Thr Lys Glu Ile Glu Val Arg Ala Val Cys Ser Asp Gly Val Gly 85 90 95

Tyr Thr Tyr Phe Thr Val Gly Gln Met Pro His Pro Val Thr Glu Arg 100 105 110
--

Asp Val Ser Gly Gly Ser Ser Asn Lys Ile Pro Ser Arg Ser Arg Gly 115 120 125
--

Ser Ala Glu Pro Leu Ser Gly Ala Cys Gly Tyr Lys Asn Gln Val 130 135 140
--

<210> SEQ ID NO 115

<211> LENGTH: 216

<212> TYPE: PRT

<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 115

Leu Phe Asp Thr Thr Met Gln Phe Glu Ile Glu Ile Ser Asn Gly Asn 1 5 10 15
--

Gln Leu Tyr Ser Ser Arg Asn Gln Leu Ile Leu Pro Gly Leu Thr Asp 20 25 30

Val Tyr Tyr His Tyr Val Ser Thr Ser Gly Pro Phe Gly Glu Asp His 35 40 45

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Pro His Asp Ile Lys Leu His Thr Thr Val His Asn Tyr Asn Pro Asn
 50          55          60

Leu Ala Val Phe Val Ile Gln Arg Glu Gly Thr Glu Leu Asn Lys Ile
65          70          75          80

Ala Phe Arg Leu Gln Val Tyr Val Leu Lys Ala Thr Thr Phe Gly Ala
85          90          95

Gly Glu His Ile Ala Glu Val Asn Phe Ile Lys Pro Lys Gly Cys Gly
100         105         110

Asp Gly Lys Arg Ser Val Asp Thr Thr Val Val Glu Pro Asn Glu Pro
115         120         125

Val Asn Lys Arg Ala Arg Thr Pro Ser Pro Ala Pro Val Asp Gln Asp
130         135         140

Leu Pro Glu Pro Lys Pro Glu Pro Glu Ser Ala Ala Glu Pro Gly Pro
145         150         155         160

Glu Leu Pro Asp Met Pro Thr Asp Asp Ala Gln Leu Glu His Glu Pro
165         170         175

Glu Pro Asp Pro Lys Pro Glu Pro Glu Ser Asp Ser Arg Glu
180         185         190

Pro Val Pro Ala Ala Pro Val Val Ala Pro Val Asp Gly His Val Asp
195         200         205

Glu Ser Pro Gln Leu Val Glu Val
210         215

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<210> SEQ ID NO 116
<211> LENGTH: 61
<212> TYPE: PRT
<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 116

Met Cys Lys Ser Thr Arg Ser Leu Cys Leu Val Lys Phe Tyr Gln Arg
 1          5          10          15

Pro Val Pro Glu Val Ser Cys Lys Leu Ala Pro Leu Asp Arg Val Met
20          25          30

Glu Val Gln Trp Ser Pro Gln Ile Asn Tyr Ser Gln Thr Lys Arg Phe
35          40          45

Trp Ser Trp Ser Trp Pro Cys Arg Gly Pro Ile Val Asn
50          55          60

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<210> SEQ ID NO 117
<211> LENGTH: 7212
<212> TYPE: DNA
<213> ORGANISM: mosquito baculovirus
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1726)....(3363)
<221> NAME/KEY: CDS
<222> LOCATION: (3384)....(4094)
<221> NAME/KEY: CDS
<222> LOCATION: (5656)....(6351)
<221> NAME/KEY: CDS
<222> LOCATION: (5206)....(5646)
<221> NAME/KEY: CDS
<222> LOCATION: (6354)....(6740)
<221> NAME/KEY: CDS
<222> LOCATION: (406)....(717)
<221> NAME/KEY: CDS
<222> LOCATION: (170)....(385)
<221> NAME/KEY: CDS
<222> LOCATION: (1519)....(1722)

<400> SEQUENCE: 117

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1	
ggc gcc gaa tgt ggt cgc ttt aag gac gta cac ttg cag acg aaa agc Gly Ala Glu Cys Gly Arg Phe Lys Asp Val His Gln Thr Lys Ser	226
5 10 15	
gat ctt att gag ctc cgt gcc ctc gcg ctg aat cac aaa gac cgc caa Asp Ile Glu Leu Arg Ala Leu Ala Leu Asn His Lys Asp Arg Gln	274
20 25 30 35	
att cgg gtt gta att gtt tac ggt cgt gtt cag ctt gat gtc gtt cgg Ile Arg Val Val Ile Val Tyr Gly Arg Val Gln Leu Asp Val Val Arg	322
40 45 50	
gtg gtc ctc acc aaa ggg tcc act cgt gct tac ata gtt ata gta cac Val Val Leu Thr Lys Gly Ser Thr Arg Ala Tyr Ile Val Ile Val His	370
55 60 65	
gtc ggt gag ccc ggg taaaattagt tggtgcgcg atg agt aca act ggt tac Val Gly Glu Pro Gly Met Ser Thr Thr Gly Tyr	423
70 75	
cgt tgc gga tct caa tct caa act gca ttg tcg tat cga aca aaa agt Arg Cys Gly Ser Gln Ser Gln Thr Ala Leu Ser Tyr Arg Thr Lys Ser	471
80 85 90	
tcc tcg atg ttc ttc gta aaa acg ttc cac aac tcg gga ctg ggg ttg Ser Ser Met Phe Phe Val Lys Thr Phe His Asn Ser Gly Leu Gly Leu	519
95 100 105 110	
cgc ttt ccg cgt ata ttc tgg gtc ata gat ttt aac gac tta atg tcc Arg Phe Pro Arg Ile Phe Trp Val Ile Asp Phe Asn Asp Leu Met Ser	567
115 120 125	
acc gcc tta tcc tca ccg tcc cgc ttg ata acg gtt ttg cgg tat aga Thr Ala Leu Ser Ser Pro Ser Arg Leu Ile Thr Val Leu Arg Tyr Arg	615
130 135 140	
aag gac cgt ttg aac tgc tcg att ggg atg cag aag atg tgc cta tcc Lys Asp Arg Leu Asn Cys Ser Ile Gly Met Gln Lys Met Cys Leu Ser	663
145 150 155	
atg acc gtc ccc gta acg cgg ttc gtc agt tta cag acc gcc ata tgg Met Thr Val Pro Val Thr Arg Phe Val Ser Leu Gln Thr Ala Ile Trp	711
160 165 170	
tcc ggg tagtacgggc aaatgcac gctgtggatg attttcgatg cggccatgg Ser GLY	767
175	
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cgtcacgttc ggtaacagg tgaggcattt gaccgaccgt gaagtaagtg tatccaactc	1427
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acg gcc ggt aaa cct tac aag cgg ttt gag cag tcg ccg ttt gtt aca Thr Ala Gly Lys Pro Tyr Lys Arg Phe Glu Gln Ser Pro Phe Val Thr 185 190 195	1587
atg tcc cgc tct gaa tac gaa ctg cga acc gca cct aac gca aac aat Met Ser Arg Ser Glu Tyr Glu Leu Arg Thr Ala Pro Asn Ala Asn Asn 200 205 210 215	1635
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ctc tgg gcg ccc gta cac ggc cag gtt gtt tta tac gac taa atg aat Leu Trp Ala Pro Val His Gly Gln Val Val Leu Tyr Asp Met Asn 235 240 245	1731
cga agc tcg aga gcc gag ggt cta cgt gaa gcc ggt ggc gtt aaa ggc Arg Ser Ser Arg Ala Glu Gly Leu Arg Glu Ala Gly Gly Val Lys Gly 250 255 260	1779
cgc cca aaa tca cgc gcc act aca acc atc aaa gct ggt aga cgc gtg Arg Pro Lys Ser Arg Ala Thr Thr Ile Lys Ala Gly Arg Pro Val 265 270 275	1827
cgc cca gct cgg cag cga caa gtt gat gaa att tta aac caa gat gaa Arg Pro Ala Arg Gln Arg Gln Val Asp Glu Ile Leu Asn Gln Asp Glu 280 285 290	1875
aat gac gat gta gca cca cct gta gcc gag ccc cag cta aat ttg gat Asn Asp Asp Val Ala Pro Pro Val Ala Glu Pro Gln Leu Asn Leu Asp 295 300 305 310	1923
gat aat gtt tgg acc ggt ggt gct acg agt ggt gat caa aat gtg gcc Asp Asn Val Trp Thr Gly Gly Ala Thr Ser Gly Asp Gln Asn Val Ala 315 320 325	1971
cca ggt tca ccc acg ggt ccc gtg gca atg tcg gtg ata tcg aag cgt Pro Gly Ser Pro Thr Gly Pro Val Ala Met Ser Val Ile Ser Lys Arg 330 335 340	2019
ctc gtg agc gag tgg cac tcg gac gga gaa ggt gag gat gaa ggt ggg Leu Val Ser Glu Trp His Ser Asp Gly Glu Gly Glu Asp Glu Gly Gly 345 350 355	2067
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aac ttc gac atg gcg tcc gag gtgcaa agt act gat gcc gct aag gtg Asn Phe Asp Met Ala Ser Glu Val Gln Ser Thr Asp Ala Ala Lys Val 425 430 435	2307
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aac aac ttt ggt gcg gca cca tcc ggt agc gga acc aca ccg cca acc Asn Asn Phe Gly Ala Ala Pro Ser Gly Ser Gly Thr Thr Pro Pro Thr 455 460 465 470	2403
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ccg gag aat tta aac gac att att acg gac cag ttg cgc gat ttc atg Pro Glu Asn Leu Asn Asp Ile Ile Thr Asp Gln Leu Arg Asp Phe Met 490 495 500	2499
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tca acg gtt ggt gag tcg aaa agt gcg ctc gca att acg gtt gcc gat Ser Thr Val Gly Glu Ser Lys Ser Ala Leu Ala Ile Thr Val Ala Asp 520 525 530	2595
cgc gtg agc aga tcg ttc atg tac gag ggt cgt att gtc gac tat aac Arg Val Ser Arg Ser Phe Met Tyr Glu Gly Arg Ile Val Asp Tyr Asn 535 540 545 550	2643
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ctg ctc tcg ttc cgc acg aaa acc tac ata atc gcc gaa ggt gta ccg Leu Leu Ser Phe Arg Thr Lys Thr Tyr Ile Ile Ala Glu Gly Val Pro 570 575 580	2739
cac gac tcg aag gtg cac gac tat gtg gac ctg acc cag tat cgg gaa His Asp Ser Lys Val His Asp Tyr Val Asp Leu Thr Gln Tyr Arg Glu 585 590 595	2787
acc gtg ccg tat tca att gcc ctc aac aac ctg agc cgc ggt gtg gac Thr Val Pro Tyr Ser Ile Ala Leu Asn Asn Leu Ser Arg Gly Val Asp 600 605 610	2835
cag gcc aac acg ctc cag ctg gcc gag ggg tgc ttg gag cag ctg aat Gln Ala Asn Thr Leu Gln Leu Ala Glu Gly Cys Leu Glu Gln Leu Asn 615 620 625 630	2883
atg gca aaa att ttc aaa gat ttc aac gaa aac att gtg ccc aac aac Met Ala Lys Ile Phe Lys Asp Phe Asn Glu Asn Ile Val Pro Asn Asn 635 640 645	2931
ctg cac aag cac aag ccc acc ttc ttc tat gcg aaa att atg aag ctg Leu His Lys His Pro Thr Phe Tyr Ala Lys Ile Met Lys Leu 650 655 660	2979
ttt gca cga ctg gtg gat agg gtg gac aat gag acg atg act gcg gtc Phe Ala Arg Leu Val Asp Arg Val Asp Asn Glu Thr Met Thr Ala Val 665 670 675	3027
gag aag cgt ttg ttt cta atg tca caa cgg ttg atc cat tgt atc cca Glu Lys Arg Leu Phe Leu Met Ser Gln Arg Leu Ile His Cys Ile Pro 680 685 690	3075
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ttc ggg aac cac ctc gag cag cgc aac cgc gag ctg aat gtg att ctg Phe Gly Asn His Leu Glu Gln Arg Asn Arg Glu Leu Asn Val Ile Leu 760 765 770	3315
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815		
tat gac cggtt acg aaa atc agg tta ttg aag gag ctg acg cgt ttc ctg Tyr Asp Arg Tyr Lys Ile Arg Leu Leu Lys Glu Leu Thr Arg Phe Leu 820	825	3512
830		
tgc ggt gaa acg gat aag gtt gac ggt gcc acg agt gaa gct aaa gcg Cys Gly Glu Thr Asp Lys Val Asp Gly Ala Thr Ser Glu Ala Lys Ala 835	840	3560
845		
gat tgt ggg ggc aag tac acg gat gaa gag cgc aag ctg ttt ggg ttt Asp Cys Gly Gly Lys Tyr Thr Asp Glu Glu Arg Lys Leu Phe Gly Phe 850	855	3608
860	865	
aaa tcg aag cag gtg att gac gat gaa agg ttg tcc agg ctg ctg gag Lys Ser Lys Gln Val Ile Asp Asp Glu Arg Leu Ser Arg Leu Leu Glu 870	875	3656
880		
gat aac aag ttg ctg tac tct gcg gtg agt gag cgt gat gcg gcg aaa Asp Asn Lys Leu Leu Tyr Ser Ala Val Ser Glu Arg Asp Ala Ala Lys 885	890	3704
895		
cgt gag cgc atg gag cag ctg aag cgg gag gaa atg gag ctc aag agt Arg Glu Arg Met Glu Gln Leu Lys Arg Glu Glu Met Glu Leu Lys Ser 900	905	3752
910		
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925		
tct gaa aac ttt ctt tcg atg gac ccc aag ttg cgc gac aag ttg atc Ser Glu Asn Phe Leu Ser Met Asp Pro Lys Leu Arg Asp Lys Leu Ile 930	935	3848
940	945	
gat cac acc gtc ata ttg gaa cca cag tac gac att ttg gcc ctg tcc Asp His Thr Val Ile Leu Glu Pro Gln Tyr Asp Ile Leu Ala Leu Ser 950	955	3896
960		
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975		
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1005		
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1020	1025	
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agt acg gac tc当地 agt tca cct caa cag cca cct aaa ccc gag ccc gga Ser Ser Asp Ser Ser Pro Gln Gln Pro Pro Lys Pro Glu Pro Gly	5793
1205 1210 1215 1220	
ccc aat acc gaa gat ccc ggc gat gag gag gtc gaa gag aat caa acg Pro Asn Thr Glu Asp Pro Gly Asp Glu Glu Val Glu Glu Asn Gln Thr	5841
1225 1230 1235	
ttc ggt gcg gcc ctc gag ctc acc gac aaa acg ctc atc aac ttg acc Phe Gly Ala Ala Leu Glu Leu Thr Asp Lys Thr Leu Ile Asn Leu Thr	5889
1240 1245 1250	
aac agt gac ctg gtc gtc aaa acc cc当地 gct cga aat aca atc caa Asn Ser Asp Leu Val Val Leu Lys Thr Pro Ala Arg Asn Thr Ile Gln	5937
1255 1260 1265	

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atg gcc gca caa gct gcg ctt caa gtc gaa tcg gaa ctg gtt tgc gtg Met Ala Ala Gln Ala Ala Leu Gln Val Glu Ser Glu Leu Val Cys Val 1270 1275 1280	5985
ggc caa gtt tcg ttg ggc tcg aac gac cag gtc gtg ttc cgt aac gca Gly Gln Val Ser Leu Gly Ser Asn Asp Gln Val Val Phe Arg Asn Ala 1285 1290 1295 1300	6033
cat gtg cac gta acg gcg gtg ccg cta aca tct gga ccc tcg ttc ttc His Val His Val Thr Ala Val Pro Leu Thr Ser Gly Pro Ser Phe Phe 1305 1310 1315	6081
tac gct aca cgt tcg gag cac ccg aga ccg gta gcg tgc gaa tcg ggg Tyr Ala Thr Arg Ser Glu His Pro Arg Pro Val Ala Cys Glu Ser Gly 1320 1325 1330	6129
tgc aaa atc gtg cgc gat aat gcc cac aag ttg acg ata att ttc tat Cys Lys Ile Val Arg Asp Asn Ala His Lys Leu Thr Ile Ile Phe Tyr 1335 1340 1345	6177
ccc gac ttg tcg ccc aac gtg tcc aca tgt ctg gac tgt atc gac ccg Pro Asp Leu Ser Pro Asn Val Ser Thr Cys Leu Asp Cys Ile Asp Pro 1350 1355 1360	6225
gaa agc gac cac gac gtg gtc atc gtg ctg agc aag gct cag gcc gac Glu Ser Asp His Asp Val Val Ile Val Leu Ser Lys Ala Gln Ala Asp 1365 1370 1375 1380	6273
atc gca aca ctt gcc gcg cta atg gcc aga aag ttt ata tat aaa gca Ile Ala Thr Leu Ala Ala Leu Met Ala Arg Lys Phe Ile Tyr Lys Ala 1385 1390 1395	6321
ccc cac att ttt acc cac aca ttc gcc caa ta atg cct ttc cga gtg Pro His Ile Phe Thr His Thr Phe Ala Gln Met Pro Phe Arg Val 1400 1405 1410	6368
aag ttc tac cca cga tcc ctc aag tat ttc gag ctt agc ccg gac tcg Lys Phe Tyr Pro Arg Ser Leu Lys Tyr Phe Glu Leu Ser Pro Asp Ser 1415 1420 1425	6416
ctc gag tac aca att tgc tgc gat gac gag tat cac cgg ttg gag acc Leu Glu Tyr Thr Ile Cys Cys Asp Asp Glu Tyr His Arg Leu Glu Thr 1430 1435 1440	6464
gag ctg tac act gac gct gga acg tac gtg tac gag aac ttc acg gtg gac Glu Leu Tyr Ser Asp Ala Gly Thr Tyr Val Tyr Glu Phe Thr Val Asp 1445 1450 1455	6512
tcg ggc tgt aaa gtt tgc gac gtt gaa gcg ttt ctg gtc aga ttc atg Ser Gly Cys Lys Val Cys Asp Val Glu Ala Phe Leu Val Arg Phe Met 1460 1465 1470 1475	6560
ttg aac tcg gaa aag aat att gac ctg tac gct gcg gag gat ttg gag Leu Asn Ser Glu Lys Asn Ile Asp Leu Tyr Ala Ala Glu Asp Leu Glu 1480 1485 1490	6608
tat tac ggg tgc gcc cac gat acc aag cat cgc gaa gct gaa aag tac Tyr Tyr Gly Cys Ala His Asp Thr Lys His Arg Glu Ala Glu Lys Tyr 1495 1500 1505	6656
aac tct gga ggt gaa tac tac tat acg ccg atg aag cga gtg cca agt Asn Ser Gly Gly Glu Tyr Tyr Tyr Thr Pro Met Lys Arg Val Pro Ser 1510 1515 1520	6704
ggc ata gct aga tgt agg att tgt gat aga aaa tct taaccatcaa Gly Ile Ala Arg Cys Arg Ile Cys Asp Arg Lys Ser 1525 1530 1535	6750
aataaacat atataaaaa ttatataaaag ttttatattttt ttgaaccgtt gaccgtttaa	6810
tttgtataact ttctgaactc gggatcgaac acctctggct ctgcaaactc gtcgtcggtc	6870
gtgcaatcgt ttctctgaa ggtgggttgc acgacacctgg cccgcgtcgg tccaccgtca	6930
tcgtcgctgt cgtcttcttc aaagcagatc tgtatattgt gcacatccccacacga	6990
tgttaggcga aaagtgtgtaa gaatacggcg gtgaacatgg ccacgctaag gtcagcgct	7050

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atgcgaggg ccgatgtgtc cgagaggcag ggcatttgc tgctgtcac cacaattctg	7110
taggttaacc tttccctgg ccgcgtcag atgttcagct tcatagtcgct cggggccggc	7170
ttcggttgg ttaaccaaat gactgtaaaa atactgctgc ag	7212

<210> SEQ ID NO 118
<211> LENGTH: 72
<212> TYPE: PRT
<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 118

Met Phe Thr Gly Ala Glu Cys Gly Arg Phe Lys Asp Val His Leu Gln			
1	5	10	15
Thr Lys Ser Asp Leu Ile Glu Leu Arg Ala Leu Ala Leu Asn His Lys			
20	25	30	
Asp Arg Gln Ile Arg Val Val Ile Val Tyr Gly Arg Val Gln Leu Asp			
35	40	45	
Val Val Arg Val Val Leu Thr Lys Gly Ser Thr Arg Ala Tyr Ile Val			
50	55	60	
Ile Val His Val Gly Glu Pro Gly			
65	70		

<210> SEQ ID NO 119
<211> LENGTH: 104
<212> TYPE: PRT
<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 119

Met Ser Thr Thr Gly Tyr Arg Cys Gly Ser Gln Ser Gln Thr Ala Leu			
1	5	10	15
Ser Tyr Arg Thr Lys Ser Ser Met Phe Phe Val Lys Thr Phe His			
20	25	30	
Asn Ser Gly Leu Gly Leu Arg Phe Pro Arg Ile Phe Trp Val Ile Asp			
35	40	45	
Phe Asn Asp Leu Met Ser Thr Ala Leu Ser Ser Pro Ser Arg Leu Ile			
50	55	60	
Thr Val Leu Arg Tyr Arg Lys Asp Arg Leu Asn Cys Ser Ile Gly Met			
65	70	75	80
Gln Lys Met Cys Leu Ser Met Thr Val Pro Val Thr Arg Phe Val Ser			
85	90	95	
Leu Gln Thr Ala Ile Trp Ser Gly			
100			

<210> SEQ ID NO 120
<211> LENGTH: 68
<212> TYPE: PRT
<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 120

Met Glu Thr Ile Arg Leu Val Thr Ala Gly Lys Pro Tyr Lys Arg Phe			
1	5	10	15
Glu Gln Ser Pro Phe Val Thr Met Ser Arg Ser Glu Tyr Glu Leu Arg			
20	25	30	
Thr Ala Pro Asn Ala Asn Asn Asp Tyr Ser Phe Val Met Arg Met Gly			
35	40	45	
Asn Lys Thr Arg Ile Val Asn Leu Trp Ala Pro Val His Gly Gln Val			
50	55	60	
Val Leu Tyr Asp			

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<210> SEQ ID NO 121
<211> LENGTH: 546
<212> TYPE: PRT
<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 121

Met Asn Arg Ser Ser Arg Ala Glu Gly Leu Arg Glu Ala Gly Gly Val
 1           5          10          15

Lys Gly Arg Pro Lys Ser Arg Ala Thr Thr Ile Lys Ala Gly Arg
 20          25          30

Pro Val Arg Pro Ala Arg Gln Arg Gln Val Asp Glu Ile Leu Asn Gln
 35          40          45

Asp Glu Asn Asp Asp Val Ala Pro Pro Val Ala Glu Pro Gln Leu Asn
 50          55          60

Leu Asp Asp Asn Val Trp Thr Gly Gly Ala Thr Ser Gly Asp Gln Asn
 65          70          75          80

Val Ala Pro Gly Ser Pro Thr Gly Pro Val Ala Met Ser Val Ile Ser
 85          90          95

Lys Arg Leu Val Ser Glu Trp His Ser Asp Gly Glu Gly Glu Asp Glu
100         105          110

Gly Gly Gln Asp Asn Asp Pro Glu Pro Glu Ser Val Ala Lys Val Asp
115         120          125

Asp Phe Leu Phe Pro Glu Leu Glu Asp Gly Pro Asp Ser Val Gly
130         135          140

Gly Ile Gly Asn Val Ser Gly Ser Val Phe Glu Val Val Gly Gly Gly
145         150         155         160

Pro Glu Gly Asp Tyr Ala Ala Gly Glu Glu Asp Glu Val Ser Arg Asn
165         170         175

Ser Leu Asn Phe Asp Met Ala Ser Glu Val Gln Ser Thr Asp Ala Ala
180         185         190

Lys Val Met Glu Leu Phe Asn Ala Leu Ser Glu Glu Gln Arg Asn Val
195         200         205

Ile Leu Asn Asn Phe Gly Ala Ala Pro Ser Gly Ser Gly Thr Thr Pro
210         215         220

Pro Thr Ser Ala Gln Pro Asp Met Glu Val Glu Asp Val Glu Thr Val
225         230         235         240

Glu Lys Pro Glu Asn Leu Asn Asp Ile Ile Thr Asp Gln Leu Arg Asp
245         250         255

Phe Met Ala Gln Glu Leu Lys Lys Ala Ala Glu Asn Tyr Val Pro Lys
260         265         270

Trp Gly Ser Thr Val Gly Glu Ser Lys Ser Ala Leu Ala Ile Thr Val
275         280         285

Ala Asp Arg Val Ser Arg Ser Phe Met Tyr Glu Gly Arg Ile Val Asp
290         295         300

Tyr Asn Gln Val Val Leu His Ile Leu Asp Asn Tyr Asp Gln Arg Leu
305         310         315         320

Glu Glu Leu Leu Ser Phe Arg Thr Lys Thr Tyr Ile Ile Ala Glu Gly
325         330         335

Val Pro His Asp Ser Lys Val His Asp Tyr Val Asp Leu Thr Gln Tyr
340         345         350

Arg Glu Thr Val Pro Tyr Ser Ile Ala Leu Asn Asn Leu Ser Arg Gly
355         360         365

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Val Asp Gln Ala Asn Thr Leu Gln Leu Ala Glu Gly Cys Leu Glu Gln
370 375 380

Leu Asn Met Ala Lys Ile Phe Lys Asp Phe Asn Glu Asn Ile Val Pro
385 390 395 400

Asn Asn Leu His Lys His Lys Pro Thr Phe Phe Tyr Ala Lys Ile Met
405 410 415

Lys Leu Phe Ala Arg Leu Val Asp Arg Val Asp Asn Glu Thr Met Thr
420 425 430

Ala Val Glu Lys Arg Leu Phe Leu Met Ser Gln Arg Leu Ile His Cys
435 440 445

Ile Pro Leu Val Ile Ile Gly Leu Thr Phe Ala Ser Lys Tyr Arg Thr
450 455 460

Ser Lys Ile Asp Cys Glu Ala Leu Ala Leu Tyr Ala Val Asn His Ala
465 470 475 480

Leu Ser Glu Lys Val Asp Lys Leu Phe Thr Phe Ala Glu Ala Gln Tyr
485 490 495

Gly Glu Pro Leu Leu Ser Arg Arg Ile Leu Ile Glu Glu Gln Ala Tyr
500 505 510

Leu Ser Phe Gly Asn His Leu Glu Gln Arg Asn Arg Glu Leu Asn Val
515 520 525

Ile Leu Asp Thr Val Leu Asn Ala Val Arg Lys Thr Tyr Arg Val Ser
530 535 540

Arg Val
545

<210> SEQ ID NO 122
<211> LENGTH: 237
<212> TYPE: PRT
<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 122

Met Gly Cys Asp Val Thr Phe Thr Leu Ile His Glu Val Tyr Ser Glu
1 5 10 15

Val Pro Val Asp Gly Lys His Val Pro Val Glu Tyr Asp Arg Tyr Lys
20 25 30

Ile Arg Leu Leu Lys Glu Leu Thr Arg Phe Leu Cys Gly Glu Thr Asp
35 40 45

Lys Val Asp Gly Ala Thr Ser Glu Ala Lys Ala Asp Cys Gly Gly Lys
50 55 60

Tyr Thr Asp Glu Glu Arg Lys Leu Phe Gly Phe Lys Ser Lys Gln Val
65 70 75 80

Ile Asp Asp Glu Arg Leu Ser Arg Leu Leu Glu Asp Asn Lys Leu Leu
85 90 95

Tyr Ser Ala Val Ser Glu Arg Asp Ala Ala Lys Arg Glu Arg Met Glu
100 105 110

Gln Leu Lys Arg Glu Glu Met Glu Leu Lys Ser Gln Thr Arg Arg Leu
115 120 125

Arg Lys Leu Asn Gln Gly Arg Leu Leu Ser Lys Ser Glu Asn Phe Leu
130 135 140

Ser Met Asp Pro Lys Leu Arg Asp Lys Leu Ile Asp His Thr Val Ile
145 150 155 160

Leu Glu Pro Gln Tyr Asp Ile Leu Ala Leu Ser Glu Tyr Asn Asp Leu
165 170 175

Val Ala Gln Lys Asp Ala Leu Glu Lys Tyr Glu Arg Met Ser Arg Arg
180 185 190

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Ser Ile Lys Asn Pro Tyr Thr Arg Ser Ala Ile Asn Ile Val Glu Arg
195 200 205

Arg Glu Gly Ala Ser Met Phe Arg Glu Lys Lys Arg Glu Asn Ile Ile
210 215 220

Asp Asn Ile Arg Gly Ile Asp Asn Ser Glu Ser Val Ala
225 230 235

<210> SEQ ID NO 123

<211> LENGTH: 147

<212> TYPE: PRT

<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 123

Met Cys Leu Leu Ser Asp Ser Arg Trp Arg Val Cys Lys Phe Ser Phe
1 5 10 15

Ala Met Ser Phe Ile Val Lys Ile Ala Leu Thr Ser Pro Glu Tyr Leu
20 25 30

Lys Asp Leu Leu Val Asn Thr Leu Glu Cys Glu Gly Val Asp Ala Asn
35 40 45

Ile Ala Ala Thr Gln Gly Ala Leu Ala Met Ala Arg Thr Leu Lys Ile
50 55 60

Ser Asn Val Arg Trp Asp Glu Pro Phe Asn Glu Asn His Gly Val Tyr
65 70 75 80

Ala Leu Leu Ser Tyr Ile Ala Thr Leu Pro Ile Tyr Ala Asn His Asp
85 90 95

Gln Val Lys Glu Ile Ala Glu Val Val Leu Trp Pro Leu Leu Ser Ala
100 105 110

Cys Thr Asn His Asp Ile Lys Phe Ala Leu Ala Ala Asn Cys Ser Ala
115 120 125

Glu Glu Arg Phe Val Ala Glu Thr Leu Arg Met Val Gly Ile Thr Val
130 135 140

Leu Glu Glu
145

<210> SEQ ID NO 124

<211> LENGTH: 232

<212> TYPE: PRT

<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 124

Met Leu Leu Gly Ser Val Ile Ile Val Ile Leu Ile Val Val Val
1 5 10 15

Phe Leu Ile Tyr Tyr Leu Leu Phe Ala Ala Ala Lys Thr Ser Ser Ser
20 25 30

Asp Ser Ser Ser Pro Gln Gln Pro Pro Lys Pro Glu Pro Gly Pro Asn
35 40 45

Thr Glu Asp Pro Gly Asp Glu Glu Val Glu Glu Asn Gln Thr Phe Gly
50 55 60

Ala Ala Leu Glu Leu Thr Asp Lys Thr Leu Ile Asn Leu Thr Asn Ser
65 70 75 80

Asp Leu Val Val Leu Lys Thr Pro Ala Arg Asn Thr Ile Gln Met Ala
85 90 95

Ala Gln Ala Ala Leu Gln Val Glu Ser Glu Leu Val Cys Val Gly Gln
100 105 110

Val Ser Leu Gly Ser Asn Asp Gln Val Val Phe Arg Asn Ala His Val
115 120 125

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His Val Thr Ala Val Pro Leu Thr Ser Gly Pro Ser Phe Phe Tyr Ala
 130 135 140
 Thr Arg Ser Glu His Pro Arg Pro Val Ala Cys Glu Ser Gly Cys Lys
 145 150 155 160
 Ile Val Arg Asp Asn Ala His Lys Leu Thr Ile Ile Phe Tyr Pro Asp
 165 170 175
 Leu Ser Pro Asn Val Ser Thr Cys Leu Asp Cys Ile Asp Pro Glu Ser
 180 185 190
 Asp His Asp Val Val Ile Val Leu Ser Lys Ala Gln Ala Asp Ile Ala
 195 200 205
 Thr Leu Ala Ala Leu Met Ala Arg Lys Phe Ile Tyr Lys Ala Pro His
 210 215 220
 Ile Phe Thr His Thr Phe Ala Gln
 225 230

<210> SEQ ID NO 125
 <211> LENGTH: 129
 <212> TYPE: PRT
 <213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 125

Met Pro Phe Arg Val Lys Phe Tyr Pro Arg Ser Leu Lys Tyr Phe Glu
 1 5 10 15
 Leu Ser Pro Asp Ser Leu Glu Tyr Thr Ile Cys Cys Asp Asp Glu Tyr
 20 25 30
 His Arg Leu Glu Thr Glu Leu Tyr Ser Asp Ala Gly Thr Tyr Val Tyr
 35 40 45
 Glu Phe Thr Val Asp Ser Gly Cys Lys Val Cys Asp Val Glu Ala Phe
 50 55 60
 Leu Val Arg Phe Met Leu Asn Ser Glu Lys Asn Ile Asp Leu Tyr Ala
 65 70 75 80
 Ala Glu Asp Leu Glu Tyr Tyr Gly Cys Ala His Asp Thr Lys His Arg
 85 90 95
 Glu Ala Glu Lys Tyr Asn Ser Gly Gly Glu Tyr Tyr Tyr Thr Pro Met
 100 105 110
 Lys Arg Val Pro Ser Gly Ile Ala Arg Cys Arg Ile Cys Asp Arg Lys
 115 120 125

Ser

<210> SEQ ID NO 126
 <211> LENGTH: 7212
 <212> TYPE: DNA
 <213> ORGANISM: mosquito baculovirus
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (708)...(944)
 <221> NAME/KEY: CDS
 <222> LOCATION: (1197)...(1364)
 <221> NAME/KEY: CDS
 <222> LOCATION: (2057)...(2242)

<400> SEQUENCE: 126

ctgcagactc	gggctcttgt	tttggttcgg	gcaaatcttg	atcgactggg	gctggactcg	60
gcgtacgggc	gcgcctgtta	accggttcgt	ttgggtcaac	gacgggtggg	tcgaccgaac	120
gttttccatc	tccgcagcct	ttaggttga	taaagttcac	ctcggcaata	tgttcaccgg	180
cggcgaatgt	ggtcgcttta	aggacgtaca	cttgcagacg	aaaagcgtac	ttattgagct	240

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ccgtgcctc	gcgctgaatc	acaaagaccg	ccaaattcgg	gttgtaattt	tgtacggtcg	300
tgtgcagtt	gatgtcgtgc	gggtggctt	caccaaaggg	tccactcgta	cttacatagt	360
gatagtacac	gtcggtgagc	ccgggtaaaa	tttagttggtt	gcccgtatgg	tacaactgg	420
taccgttgcg	gatctcaatc	tcaaaactgca	ttgtcgtatc	gaacaaaaag	ttcctcgatg	480
ttcttcgtaa	aaacgttcca	caactcgaaa	ctgggggtgc	gctttcccg	tatattctgg	540
gtcatagatt	ttaacgactt	aatgtccacc	gccttatctt	caccgtcccc	cttgataacg	600
gttttgcgtt	atagaaagga	ccggttgaac	tgctcgattt	ggatgcagaa	gatgtgccta	660
tccatgaccg	tccccgtaac	gcccgtcg	agtttacaga	ccggccat	atg gtc cgg	716
				Met Val Arg		
			1			
gta gta	cg	gca aat	gcc aac	gct gtg	gat gat	764
Val Val	Arg	Ala Asn	Ala Asn	Ala Val	Asp Asp	Phe Arg Cys Gly His
5	10	15				
ggt tgc	gct gag	caa atc	gct gtt acc	aat cag	gca ggt	812
Gly Cys	Ala Glu	Gln Ile	Ala Val	Thr Asn	Gln Ala	Gly Tyr Glu Arg
20	25	30	35			
gat ggc	aat caa	cac ggc	cct gta	gta gcg	gta att tac	860
Asp Gly	Asn Gln	His Gly	Pro Val	Val Ala	Val Ile	Tyr Tyr His Leu
40	45	50				
gtc gtc	cag tgg	gta gcc	gcg cga	gac cag	tgg gta	908
Val Val	Gln Trp	Val Ala	Ala Arg	Asp Gln	Trp Val	Leu Glu Ile Phe
55	60	65				
aac gaa	ggg gtg	tat aat	gag gag	gtc ctg	tgg tgc	954
Asn Glu	Gly Val	Tyr Asn	Glu Glu	Val Val	Trp Cys	
70	75					
gattccgcgc	taacgtacaa	ctctagcgcc	gagttggcg	aaattaaaaat	ttgtctatct	1014
agcgttctgt	atatcggtc	aatgtcatcg	taaacgtggc	caatgtttat	aactctaccc	1074
ccaaagctgg	agcggAACAG	gtccagggtc	aaccgcagca	cacaattgtat	cttggggac	1134
gcgtataaac	aggcgtaac	tgtacctcg	ttttccctgc	acatgccccat	caggcccaca	1194
ta atg	gtg cac	cat gtt	cga gtt	ccc cat	cga gag	1241
Met Val	His His	Val Arg	Gln Val	Pro His	Arg Glu Phe	Gly
80	85	90				
gac gtg	agt ttt	gct gta	gtt ttt	gat gaa	aat ttt	1289
Asp Val	Ser Phe	Ala Val	Val Phe	Asp Glu	Asn Phe	Thr Leu Asp Phe
95	100	105	110			
tgt atc	cac atg	cac cgg	aca ggg	gtt ccg	ccg acc ctc	1337
Cys Ile	His Met	His Arg	Thr Gly	Val Pro	Pro Thr	Leu Ala Thr Gly
115	120	125				
ttg gga	ttt tgt	tgc atg	aac cgc	cgc taacgtcacg	ttcggttaaca	1384
Leu Gly	Phe Cys	Ser Met	Asn Arg			
130	135					
gggtgaggca	tttgaccgac	cgtgaagtaa	gtgtatccaa	ctccatca	gaaaactgc	1444
cgaactcaa	tctccttcgt	ctccggattt	attataaccc	tttgcgcag	aaaagtctcg	1504
gtaaacgcac	ccatatggaa	acaattcgcc	tcgttacggc	cggtaaacct	tacaagcggt	1564
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acgcaaacaa	tgactactct	tgcgtatgc	gaatgggtaa	taagacacgt	attgtgaacc	1684
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ccgagggtct	acgtgaagcc	ggtggcggtt	aaggccgccc	aaaatcacgc	gccactacaa	1804
ccatcaaagc	tggtagaccg	gtgcgcccag	ctcgccagcg	acaagttgat	gaaattttaa	1864
accaagatga	aatgacat	gtagcaccac	ctgttagccga	gccccagcta	aatttggatg	1924

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ataatgtttg gaccgggtgt gctacgagtg gtgatcaaaa tgtggcccca ggttcaccca 1984
cgggtcccggt ggcaatgtcg gtgatatcga agcgtctcg gagcgagtgg cactcgacg 2044
gagaaggtga gg atg aag gtg ggc agg ata acg atc ccg agc ccg agt cg 2095
Met Lys Val Gly Arg Ile Thr Ile Pro Ser Pro Ser Arg
140 145
tgg cca agg tgg acg act ttt tat ttc ccg agc tcg agg aag acg gac 2143
Trp Pro Arg Trp Thr Thr Phe Tyr Phe Pro Ser Ser Arg Lys Thr Asp
150 155 160
cg act cg ttg gcg gaa ttg gca acg ttt ctg gtt cag ttt tcg aag 2191
Arg Thr Arg Leu Ala Glu Leu Ala Thr Phe Leu Val Gln Phe Ser Lys
165 170 175 180
ttg tcg gtg gtg gcc ccg agg gcg act atg ctg ctg gtg agg agg acg 2239
Leu Ser Val Val Ala Pro Arg Ala Thr Met Leu Leu Val Arg Arg Thr
185 190 195
aag taagcagaaa ttcgctaaac ttcgacatgg cgtccgaggt gcaaagtact 2292
Lys
gatgccgcta aggtgatgga gctgttaac gccctatccg aggagcagcg aaatgtgatt 2352
ctaaacaact ttggcgcc accatccggt agcggAACCA caccgccaac ctcggctcaa 2412
cccgatatgg aggtttaggaa tggttagact gtggaaaagc cggagaattt aaacgacatt 2472
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gaagctttgg ccctgtacgc cgtgaaccat gcgtgtctg aaaagggttgg taaattgttc 3192
acatttgcgg aagcacagta cggtaaccg ctgctcagcc gccgtatact aattgaagag 3252
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accgattaaa gatgggtcgc gacgtaacgt tcacccgttccatccgatccggatgttattgtt 3432
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ctaaagcgga ttgtgggggc aagtacacgg atgaagagcg caagctgttt gggtttaat 3612
cgaagcaggt gattgacatg gaaagggtgtt ccaggctgtccggatccaaac aagttgtgtt 3672
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aggaaatggc gctcaagagt ccaaaccggaa gattgcgcac actgaaccag ggtcggttgc 3792
tgtccaaatgc tggaaactttt ctttcgtatgg accccaaatgtt ggcgcacaag ttgtatcgatc 3852
acaccgtcat attggaaacca cagtagcaca ttttggccct gtcggatgtat aacgatttgg 3912
tagcgcacaaa ggtgcctc gagaagtgacg aacgaaatgtc cagacgtcg ataaagaatc 3972

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cgtacacccg ctccgccata aacatcggtt agcgcggta ggggcgtca atgttccgtg	4032
agaagaagcg cggaaacatt attgacaaca tacgcggat cgacaatagc gaaagtgtag	4092
cgtgatatat ttttgaataa taaatatata aaataataa atagataaat aaataaatgt	4152
ttctggttga aattaacca tattttat cgttgatca cacgtaccca tagtaattat	4212
atataaaaaaaa aaaagtccaa tgaatttat tggccctgg aataacttag cggtggacca	4272
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<210> SEQ ID NO 127

<211> LENGTH: 79

<212> TYPE: PRT

<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 127

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Cys Gly His Gly Cys Ala Glu Gln Ile Ala Val Thr Asn Gln Ala Gly	
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Tyr Glu Arg Asp Gly Asn Gln His Gly Pro Val Val Ala Val Ile Tyr	
35 40 45	

Tyr His Leu Val Val Gln Trp Val Ala Ala Arg Asp Gln Trp Val Leu	
50 55 60	

Glu Ile Phe Asn Glu Gly Val Tyr Asn Glu Glu Val Leu Trp Cys	
65 70 75	

<210> SEQ ID NO 128

<211> LENGTH: 56

<212> TYPE: PRT

<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 128

Met Val His His Val Arg Val Gln Val Pro His Arg Glu Phe Gly Asp	
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Val Ser Phe Ala Val Val Phe Asp Glu Asn Phe Thr Leu Asp Phe Cys	
20 25 30	

Ile His Met His Arg Thr Gly Val Pro Pro Thr Leu Ala Thr Gly Leu	
35 40 45	

Gly Phe Cys Ser Met Asn Arg Arg	
50 55	

<210> SEQ ID NO 129

<211> LENGTH: 62

<212> TYPE: PRT

<213> ORGANISM: mosquito baculovirus

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<400> SEQUENCE: 129

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Trp Thr Thr Phe Tyr Phe Pro Ser Ser Arg Lys Thr Asp Arg Thr Arg
 20          25          30
Leu Ala Glu Leu Ala Thr Phe Leu Val Gln Phe Ser Lys Leu Ser Val
 35          40          45
Val Ala Pro Arg Ala Thr Met Leu Leu Val Arg Arg Thr Lys
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<210> SEQ ID NO 130

<211> LENGTH: 7212

<212> TYPE: DNA

<213> ORGANISM: mosquito baculovirus

<220> FEATURE:

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Met Lys Leu Asn Ile Ser Ala Arg Pro Gly Lys Arg Leu Thr Tyr Arg
 1           5          10          15
att gtg gtg cac gac agc aaa atg ccc tgc ctc tcg gac aca tcg gcc      154
Ile Val Val His Asp Ser Lys Met Pro Cys Leu Ser Asp Thr Ser Ala
 20          25          30
ctc gca ata gcg ctg agc ctt agc gtg gca atg ttc acc gcc gta ttc      202
Leu Ala Ile Ala Leu Ser Leu Ser Val Ala Met Phe Thr Ala Val Phe
 35          40          45
tac aca ctt ttg cgc cta cat cgt gtg gag aaa aat gtg cac aat ata      250
Tyr Thr Leu Leu Arg Leu His Arg Val Glu Lys Asn Val His Asn Ile
 50           55           60
cag atc tgc ttt gaa gaa gac gac gac gat gac ggt gga ccg acg      298
Gln Ile Cys Phe Glu Glu Asp Asp Asp Asp Asp Gly Gly Pro Thr
 65           70           75           80
cgg gcc gag gtc gtg caa ccc acc ttc aga gaa aac gat tgc acg acc      346
Arg Ala Glu Val Val Gln Pro Thr Phe Arg Glu Asn Asp Cys Thr Thr
 85           90           95
gac gac gag ttt gca gag cca gag gtg ttc gat ccc gag ttc aga aag      394
Asp Asp Glu Phe Ala Glu Pro Glu Val Phe Asp Pro Glu Phe Arg Lys
100          105          110
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Tyr His Asn
 115
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120 125	
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130 135 140	
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145 150 155	
cac cag gtc act gtt ggt caa gtt gat gag cgt ttt gtc ggt gag ctc His Gln Val Thr Val Gly Gln Val Asp Glu Arg Phe Val Gly Glu Leu	1356
160 165 170 175	
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180 185 190	
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195 200 205	
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225 230 235 240	
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245 250 255	
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260 265 270	
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275 280 285	
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290 295 300	
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cca ctg caa gtt gtg cac aac gtg gtg gca aac atg tac att tcg ttg Pro Leu Gln Val Val His Asn Val Val Ala Asn Met Tyr Ile Ser Leu 405 410 415				2491
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tcc tcc agc agc ctg gac aac ctt tca tcg tca atc acc tgc ttc gat Ser Ser Ser Ser Leu Asp Asn Leu Ser Ser Ile Thr Cys Phe Asp 670 675 680	3602
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775 780 785	
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Val His Arg Thr Lys Ser Gln Ala Gly Arg Glu Gly Arg Arg Asn Pro	
790 795 800 805	
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Cys Pro Val His Val Asp Thr Lys Ile Lys Cys Lys Ile Phe Ile Lys	
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Cys Val Leu Arg Phe Asp Leu Asp Leu Phe Arg Ser Ser Phe Gly Gly	
870 875 880 885	
aga gtt ata aac att ggc cac gtt tac gat gaa ctt gac cgc ata tac	6190
Arg Val Ile Asn Ile Gly His Val Tyr Asp Glu Leu Asp Arg Ile Tyr	
890 895 900	
aga acg cta gat aga caa att tta att tcg ccc aac tcg gcg cta gag	6238
Arg Thr Leu Asp Arg Gln Ile Leu Ile Ser Pro Asn Ser Ala Leu Glu	
905 910 915	
ttg tac gtt agc gcg gaa tct ggg gtg cta gca cca cag gac ctc ctc	6286
Leu Tyr Val Ser Ala Glu Ser Ala Val Leu Ala Pro Gln Asp Leu Leu	
920 925 930	
att ata cac ccc ttc gtt gaa gat ctc gag tac cca ctg gtc tcg cgc	6334
Ile Ile His Pro Phe Val Glu Asp Leu Glu Tyr Pro Leu Val Ser Arg	

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935	940	945	
ggc tac cca ctg gac gac gag gtg ata gta aat tac cgc tac tac agg Gly Tyr Pro Leu Asp Asp Glu Val Ile Val Asn Tyr Arg Tyr Tyr Arg	950	955	6382
960			965
gcc gtg ttg att gcc atc acg ctc gta acc tgc ctg att ggt aac agc Ala Val Leu Ile Ala Ile Thr Leu Val Thr Cys Leu Ile Gly Asn Ser	970	975	6430
980			
gat ttg ctc acg aca acc atg gcc gca tcg aaa atc atc cac agc gtt Asp Leu Leu Ser Thr Thr Met Ala Ala Ser Lys Ile Ile His Ser Val	985	990	6478
995			
ggc att tgc ccg tac tac ccg gac cat atg gcg gtc tgt aaa ctg acg Gly Ile Cys Pro Tyr Tyr Pro Asp His Met Ala Val Cys Lys Leu Thr	1000	1005	6526
1010			
aac cgc gtt acg ggg acg gtc atg gat agg cac atc ttc tgc atc cca Asn Arg Val Thr Gly Thr Val Met Asp Arg His Ile Phe Cys Ile Pro	1015	1020	6574
1025			
atc gag cag ttc aaa cggttccatac tac cgc aaa acc gtt atc aag Ile Glu Gln Phe Lys Arg Ser Phe Leu Tyr Arg Lys Thr Val Ile Lys	1030	1035	6622
1040			1045
cgg gac ggt gag gat aag gcg gtg gac att aag tcg tta aaa tct atg Arg Asp Gly Glu Asp Lys Ala Val Asp Ile Lys Ser Leu Lys Ser Met	1050	1055	6670
1060			
acc cag aat ata cgc gga aag cgc aac ccc agt ccc gag ttg tgg aac Thr Gln Asn Ile Arg Gly Lys Arg Asn Pro Ser Pro Glu Leu Trp Asn	1065	1070	6718
1075			
gtt ttt acg aag aac atc gag gaa ctt ttt gtt cga tac gac aat gca Val Phe Thr Lys Asn Ile Glu Glu Leu Phe Val Arg Tyr Asp Asn Ala	1080	1085	6766
1090			
gtt tgagatttagt atccgcaacg gtaaccagggt gtactcatcg cgcaaccaac Val			6819
taattttacc cgggtcacc gacgtgtact atcactatgt aagcacgagt ggaccctttg gtgaggacca cccgacacgatcaagctgc acacgaccgt acacaattac aacccgaatt			6879
tggcggtctt tggatttcg cgcgaggcga cggagctcaa taagatcgct ttccgtctgc aagtgtacgt ccttaaagcgc accacattcg gcgcgggtga acatattgcc gaggtgaact			6939
ttatcaaacc taaaggctgc ggagatggaa aacgttcggt cgacaccacc gtcgttgaac caaacaacc ggtaacaag cgcgcggta cggcggatcc agccccagtc gatcaagatt			6999
tgcccgaaacc aaaaccagag cccgagtctg cag			7119
			7179
<210> SEQ ID NO 131			
<211> LENGTH: 115			
<212> TYPE: PRT			
<213> ORGANISM: mosquito baculovirus			
<400> SEQUENCE: 131			
Met Lys Leu Asn Ile Ser Ala Arg Pro Gly Lys Arg Leu Thr Tyr Arg 1 5 10 15			
Ile Val Val His Asp Ser Lys Met Pro Cys Leu Ser Asp Thr Ser Ala 20 25 30			
Leu Ala Ile Ala Leu Ser Leu Ser Val Ala Met Phe Thr Ala Val Phe 35 40 45			
Tyr Thr Leu Leu Arg Leu His Arg Val Glu Lys Asn Val His Asn Ile 50 55 60			
Gln Ile Cys Phe Glu Glu Asp Asp Asp Asp Asp Gly Gly Pro Thr 65 70 75 80			
Arg Ala Glu Val Val Gln Pro Thr Phe Arg Glu Asn Asp Cys Thr Thr			

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85	90	95
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Asp Asp Glu Phe Ala Glu Pro Glu Val Phe Asp Pro Glu Phe Arg Lys	100	105
		110
Tyr His Asn		
	115	

<210> SEQ_ID NO 132
<211> LENGTH: 91
<212> TYPE: PRT
<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 132

Met Cys Val Thr Glu His Asp Leu Val Val Arg Ala Gln Arg Asn Leu	1	15
	5	10

Ala His Ala Asn Gln Phe Arg Phe Asp Leu Lys Arg Ser Leu Cys Gly	20	25
		30

His Leu Asp Cys Ile Ser Ser Arg Gly Phe Glu His His Gln Val Thr	35	40
		45

Val Gly Gln Val Asp Glu Arg Phe Val Gly Glu Leu Glu Gly Arg Thr	50	55
		60

Glu Arg Leu Ile Leu Phe Asp Leu Leu Ile Ala Gly Ile Phe Gly Ile	65	70
		75
		80

Gly Ser Gly Leu Gly Phe Arg Trp Leu Leu Arg	
85	90

<210> SEQ_ID NO 133
<211> LENGTH: 370
<212> TYPE: PRT
<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 133

Met Phe Ala Ser Thr Pro Ser His Ser Ser Val Phe Thr Ser Lys Ser	1	5
		10
		15

Phe Arg Tyr Ser Gly Leu Val Ser Ala Ile Phe Thr Met Asn Asp Ile	20	25
		30

Ala Lys Glu Asn Leu Gln Thr Arg Gln Arg Glu Ser Leu Asn Arg His	35	40
		45

Ile Phe Tyr Leu Val Ile Thr Ser Leu Leu Ser Pro Thr Glu Thr Glu	50	55
		60

Ser Asn Leu Ala Lys Val Glu Phe Ala Thr Ile Val Tyr Leu Met Asn	65	70
		75
		80

Leu Ser Met Leu Leu Ala Arg Pro Pro Ala Pro Ile Val Val Ser Glu	85	90
		95

Glu Arg Val Arg Gln Phe Trp Ser Ile Tyr Gln Lys Arg Thr Lys Leu	100	105
		110

His Leu Asp Leu Ile Leu Gly Asn Lys Arg Gly Gln Asp Arg Gln Met	115	120
		125

Ala Tyr Met Ser Ser Lys Pro Glu Phe Val Ala His Tyr Asn Ser Ala	130	135
		140

Ala Lys Glu Cys Glu Leu Asp Pro Ile Ala Val Val Pro Leu Pro Tyr	145	150
		155
		160

Ile His Gly Glu His Phe His Asn Ser Trp Asp Val Met His Leu Met	165	170
		175

Ala Glu Val Gly Asp Gln Ile Val Ala Gln Arg Asn Asp Met Leu Ala	180	185
		190

Leu Ala Pro Leu Gln Val Val His Asn Val Val Ala Asn Met Tyr Ile

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195	200	205
Ser Leu Gly Cys Gln Thr	Cys Val Ser His Tyr	Leu Leu Leu Arg Gly
210	215	220
Val Ile Leu Val Lys Phe Glu Gln Leu Phe Arg	Leu Leu Val Leu Glu	
225	230	235 240
Glu Leu Lys Arg Arg Glu Gly Ser Ile Ser Gly Arg	Thr Ile Glu Leu	
245	250	255
Leu Arg Ile Pro Thr Val Glu Leu Asp Glu Tyr Ile Ala Asn Pro Gly		
260	265	270
Val Leu Asn Asn Ala Phe Val Lys Asn Leu Leu Ala Tyr Glu Met Val		
275	280	285
Gln Leu His Asn Tyr Ile Asn Ser Tyr Arg Ile Val Gln Gln Ala Ser		
290	295	300
Gly His Leu Arg Ser Asn Arg Pro Ile Glu Gln Ala Asp Ile Lys Val		
305	310	315 320
Tyr Leu Lys Ala Phe Gln Glu Gly Pro Thr Met Thr Trp Glu Leu Tyr		
325	330	335
Asp Lys Gln Arg Arg Gly Glu Ile Ala Pro Ile Ser Pro Val Arg Lys		
340	345	350
Arg Pro Ala Pro Asp Asp Ser Thr Gly Pro Pro Leu Lys Tyr Ser Arg		
355	360	365
Ala Gln		
370		

<210> SEQ ID NO 134
<211> LENGTH: 70
<212> TYPE: PRT
<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 134

Met Leu Ser Ile Met Phe Ser Arg Phe Phe Ser Arg Asn Ile Asp Ala		
1	5	10 15
Pro Ser Arg Arg Ser Thr Met Phe Met Ala Glu Arg Val Tyr Gly Phe		
20	25	30
Phe Ile Asp Arg Leu Asp Ile Arg Ser Tyr Phe Ser Arg Ala Ser Phe		
35	40	45
Cys Ala Thr Lys Ser Leu Tyr Ser Asp Arg Ala Lys Met Ser Tyr Cys		
50	55	60
Gly Ser Asn Met Thr Val		
65	70	

<210> SEQ ID NO 135
<211> LENGTH: 119
<212> TYPE: PRT
<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 135

Met Arg Ser Arg Phe Ala Ala Ser Arg Ser Leu Thr Ala Glu Tyr Ser		
1	5	10 15
Asn Leu Leu Ser Ser Ser Leu Asp Asn Leu Ser Ser Ser Ile Thr		
20	25	30
Cys Phe Asp Leu Asn Pro Asn Ser Leu Arg Ser Ser Ser Val Tyr Leu		
35	40	45
Pro Pro Gln Ser Ala Leu Ala Ser Leu Val Ala Pro Ser Thr Leu Ser		
50	55	60
Val Ser Pro His Arg Lys Arg Val Ser Ser Phe Asn Asn Leu Ile Leu		

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65	70	75	80
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Tyr Arg Ser Tyr Ser Thr Gly Thr Cys Phe Pro Ser Thr Gly Thr Ser			
85	90	95	

Glu Tyr Thr Ser Trp Ile Lys Val Asn Val Thr Ser Gln Pro Ile Phe			
100	105	110	

Asn Arg Cys Gln Leu Lys Leu			
115			

<210> SEQ ID NO 136

<211> LENGTH: 329

<212> TYPE: PRT

<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 136

Met Glu Leu Asp Thr Leu Thr Ser Arg Ser Val Lys Cys Leu Thr Leu			
1	5	10	15

Leu Pro Asn Val Thr Leu Ala Ala Val His Arg Thr Lys Ser Gln Ala			
20	25	30	

Gly Arg Glu Gly Arg Arg Asn Pro Cys Pro Val His Val Asp Thr Lys			
35	40	45	

Ile Lys Cys Lys Ile Phe Ile Lys Asn Tyr Ser Lys Thr His Val Thr			
50	55	60	

Glu Leu Ser Met Gly Tyr Leu Asn Ser Asn Met Val His His Tyr Val			
65	70	75	80

Ala Leu Met Gly Met Cys Arg Glu Asn Arg Gly Thr Val Asp Ala Cys			
85	90	95	

Leu Tyr Ala Ser Asn Lys Ile Asn Cys Val Leu Arg Phe Asp Leu Asp			
100	105	110	

Leu Phe Arg Ser Ser Phe Gly Gly Arg Val Ile Asn Ile Gly His Val			
115	120	125	

Tyr Asp Glu Leu Asp Arg Ile Tyr Arg Thr Leu Asp Arg Gln Ile Leu			
130	135	140	

Ile Ser Pro Asn Ser Ala Leu Glu Leu Tyr Val Ser Ala Glu Ser Ala			
145	150	155	160

Val Leu Ala Pro Gln Asp Leu Leu Ile Ile His Pro Phe Val Glu Asp			
165	170	175	

Leu Glu Tyr Pro Leu Val Ser Arg Gly Tyr Pro Leu Asp Asp Glu Val			
180	185	190	

Ile Val Asn Tyr Arg Tyr Tyr Arg Ala Val Leu Ile Ala Ile Thr Leu			
195	200	205	

Val Thr Cys Leu Ile Gly Asn Ser Asp Leu Leu Ser Thr Thr Met Ala			
210	215	220	

Ala Ser Lys Ile Ile His Ser Val Gly Ile Cys Pro Tyr Tyr Pro Asp			
225	230	235	240

His Met Ala Val Cys Lys Leu Thr Asn Arg Val Thr Gly Thr Val Met			
245	250	255	

Asp Arg His Ile Phe Cys Ile Pro Ile Glu Gln Phe Lys Arg Ser Phe			
260	265	270	

Leu Tyr Arg Lys Thr Val Ile Lys Arg Asp Gly Glu Asp Lys Ala Val			
275	280	285	

Asp Ile Lys Ser Leu Lys Ser Met Thr Gln Asn Ile Arg Gly Lys Arg			
290	295	300	

Asn Pro Ser Pro Glu Leu Trp Asn Val Phe Thr Lys Asn Ile Glu Glu			
305	310	315	320

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Leu Phe Val Arg Tyr Asp Asn Ala Val
325

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<210> SEQ_ID NO 137
<211> LENGTH: 7212
<212> TYPE: DNA
<213> ORGANISM: mosquito baculovirus
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (575)....(946)
<221> NAME/KEY: CDS
<222> LOCATION: (5695)....(5934)
<221> NAME/KEY: CDS
<222> LOCATION: (237)....(470)
<221> NAME/KEY: CDS
<222> LOCATION: (1)....(174)
<221> NAME/KEY: CDS
<222> LOCATION: (4295)....(4450)
<221> NAME/KEY: CDS
<222> LOCATION: (1149)....(1301)
<221> NAME/KEY: CDS
<222> LOCATION: (6747)....(7209)

<400> SEQUENCE: 137

ctg cag cag tat ttt tac agt cat ttg gtt aac caa acc gaa gcc cg 48
Leu Gln Gln Tyr Phe Tyr Ser His Leu Val Asn Gln Thr Glu Ala Arg
 1           5          10          15

ccc gac gac tat gaa gct gaa cat ctc agc gcg gcc agg gaa aag gtt 96
Pro Asp Asp Tyr Glu Ala Glu His Leu Ser Ala Ala Arg Glu Lys Val
 20          25          30

aac cta cag aat tgt ggt gca cga cag caa aat gcc ctg cct ctc gga 144
Asn Leu Gln Asn Cys Gly Ala Arg Gln Gln Asn Ala Leu Pro Leu Gly
 35          40          45

cac atc ggc cct cgc aat agc gct gag cct tagcgtggca atgttcaccg 194
His Ile Gly Pro Arg Asn Ser Ala Glu Pro
 50          55

ccgtattctca cacacttttg cgcctacatc gtgtggagaa aa atg tgc aca ata 248
Met Cys Thr Ile
 60

tac aga tct gct ttg aag aag acg acg acg atg acg gtg gac cga 296
Tyr Arg Ser Ala Leu Lys Lys Thr Thr Thr Met Thr Val Asp Arg
 65          70          75

cgc ggg ccg agg tcg tgc aac cca cct tca gag aaa acg att gca cga 344
Arg Gly Pro Arg Ser Cys Asn Pro Pro Ser Glu Lys Thr Ile Ala Arg
 80          85          90

ccg acg acg agt ttg cag acg cag agg tgt tcg atc ccg agt tca gaa 392
Pro Thr Thr Ser Leu Gln Ser Gln Arg Cys Ser Ile Pro Ser Ser Glu
 95          100         105         110

agt atc aca att aaa cgg tca acg gtt caa aat aaa tac act tta ata 440
Ser Ile Thr Ile Lys Arg Ser Thr Val Gln Asn Lys Tyr Thr Leu Ile
 115         120         125

aat ttt ata tat atc gtt tat ttt act ggt taagattttc tatcacaat 490
Asn Phe Ile Tyr Ile Val Tyr Phe Thr Gly
 130         135

cctacatcta gctatgccac ttggcactcg cttcatcgcc gtatagttagt attcacctcc 550

agagttgtac ttttcagctt cgcg atg ctt ggt atc gtg ggc gca ccc gta 601
Met Leu Gly Ile Val Gly Ala Pro Val
 140         145

ata ctc caa atc ctc cgc agc gta cag gtc aat att ctt ttc cga gtt 649
Ile Leu Gln Ile Leu Arg Ser Val Gln Val Asn Ile Leu Phe Arg Val
 150         155         160

caa cat gaa tct gac cag aaa cgc ttc aac gtc gca aac ttt aca gcc 697
Gln His Glu Ser Asp Gln Lys Arg Phe Asn Val Ala Asn Phe Thr Ala
 165         170         175

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cga gtc cac cgt gaa ctc gta cac gta cgt tcc agc gtc act gta cag	745
Arg Val His Arg Glu Leu Val His Val Arg Ser Ser Val Thr Val Gln	
180 185 190	
ctc ggt ctc caa ccg gtg ata ctc gtc atc gca gca aat tgt gta ctc	793
Leu Gly Leu Gln Pro Val Ile Leu Val Ile Ala Ala Asn Cys Val Leu	
195 200 205	
gag cga gtc cgg gct aag ctc gaa ata ctt gag gga tcg tgg gta gaa	841
Glu Arg Val Arg Ala Lys Leu Glu Ile Leu Glu Gly Ser Trp Val Glu	
210 215 220 225	
ctt cac tcg gaa agg cat tat tgg gcg aat gtg tgg gta aaa atg tgg	889
Leu His Ser Glu Arg His Tyr Trp Ala Asn Val Trp Val Lys Met Trp	
230 235 240	
ggg gct tta tat ata aac ttt ctg gcc att agc gcg gca agt gtt gcg	937
Gly Ala Leu Tyr Ile Asn Phe Leu Ala Ile Ser Ala Ala Ser Val Ala	
245 250 255	
atg tgc gcc tgagccttgc tcagcacat gaccacgtcg tggcgctt	986
Met Ser Ala	
260	
ccgggtcgat acagtccaga catgtggaca cgttggcga caagtcggga tagaaaatta	1046
tcgtcaactt gtggcattt tcgcgcacga tttgcaccc cgattcgcac gctaccggc	1106
tcgggtgctc cgaacgtgta gcgtagaaga acgagggtcc ag atg tta gcg gca	1160
Met Leu Ala Ala	
ccg ccg tta cgt gca cat gtg cgt tac gga aca cga cct ggt cgt tcg	1208
Pro Pro Leu Arg Ala His Val Arg Tyr Gly Thr Arg Pro Gly Arg Ser	
265 270 275 280	
agc cca acg aaa ctt ggc cca cgc aaa cca gtt ccg att cga ctt gaa	1256
Ser Pro Thr Lys Leu Gly Pro Arg Lys Pro Val Pro Ile Arg Leu Glu	
285 290 295	
gcg cag ctt gtg cgg cca ttt gga ttg tat ttc gag ccg ggg ttt	1301
Ala Gln Leu Val Arg Pro Phe Gly Leu Tyr Phe Glu Pro Gly Phe	
300 305 310	
tgagcaccac caggtcaactg ttggcaactg ttagtgcgt tttgtcggtg agctcgagg	1361
ccgcacccaa cgttgcattc tcttcgaccc cctcatcgcc gggatctcg gtattgggtc	1421
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tttcggctac gaatctctcc tccgcactac agttgcgc gaggcgtcaa ttaatatcg	1661
gattcggtca ggcgtttaaa agtggccata gcaccacttc ggctatctcc ttaacttgg	1721
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tcaccacccctt gttgagcccc accgaaaccg aatccaaacct cgccaaagtt gagtttgc	2081
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tcagcgaaaga acgcgtacgc caatttttgtt ccataatataca aaagcgccacc aagctgcacc	2201
tcgatttgat tctcgcaac aaacgcggc aggaccgcac gatggcgtac atgtccagca	2261
agccccgaaattt cgttgcggcatacaacagcg cggccaaaggaa gtgcgagctg gacccat	2321
cggtggtccc actaccctac attcacggtg aacatttca caactcgatgg gacgtgatgc	2381

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caccactgca agtttgac aacgtggtgg caaacatgt catttcgttg ggctgccaaa	2501
cctgcgtttc acactaccta ttgttgcccc gcgtcataact ggtaaagtcc gaacaactct	2561
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tcgagttgtc gcaatccc accgttgagc tggacgagta catgcacaa cccggcgatc	2681
tgaacaacgc ctttgttaaa aatttactag cgtacgaaat ggtccagctg cacaactata	2741
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ttt tcg ttg aaa tct ttg aaa att ttt gcc ata ttc agc tgc tcc aag Phe Ser Leu Lys Ser Leu Lys Ile Phe Ala Ile Phe Ser Cys Ser Lys 315 320 325	4345
cac ccc tcg gcc agc tgg agc gtg ttg gcc tgg tcc aca ccg cgg ctc His Pro Ser Ala Ser Trp Ser Val Leu Ala Trp Ser Thr Pro Arg Leu 330 335 340	4393
agg ttg ttg agg gca att gaa tac ggc acg gtt tcc cga tac tgg gtc Arg Leu Leu Arg Ala Ile Glu Tyr Gly Thr Val Ser Arg Tyr Trp Val 345 350 355 360	4441
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Arg Ser Thr

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aca atg cag ttt gag att gag atc cgc aac ggt aac cag ttg tac tca Thr Met Gln Phe Glu Ile Glu Ile Arg Asn Gly Asn Gln Leu Tyr Ser 450 455 460	6806
tcg cgc aac caa cta att tta ccc ggg ctc acc gac gtg tac tat cac Ser Arg Asn Gln Leu Ile Leu Pro Gly Leu Thr Asp Val Tyr Tyr His 465 470 475	6854
tat gta agc acg agt gga ccc ttt ggt gag gac cac ccg cac gac atc Tyr Val Ser Thr Ser Gly Pro Phe Gly Glu Asp His Pro His Asp Ile 480 485 490 495	6902
aag ctg cac acg acc gta cac aat tac aac ccg aat ttg gcg gtc ttt Lys Leu His Thr Val His Asn Tyr Asn Pro Asn Leu Ala Val Phe 500 505 510	6950
gtg att cag cgc gag ggc acg gag ctc aat aag atc gct ttt cgt ctg Val Ile Gln Arg Glu Gly Thr Glu Leu Asn Lys Ile Ala Phe Arg Leu 515 520 525	6998
caa gtg tac gtc ctt aaa ggc acc aca ttc ggc gcc ggt gaa cat att Gln Val Tyr Val Leu Lys Ala Thr Thr Phe Gly Ala Gly Glu His Ile 530 535 540	7046
gcc gag gtg aac ttt atc aaa cct aaa ggc tgc gga gat gga aaa cgt Ala Glu Val Asn Phe Ile Lys Pro Lys Gly Cys Gly Asp Gly Lys Arg 545 550 555	7094
tcg gtc gac acc acc gtc gtt gaa cca aac gaa ccg gtt aac aag cgc Ser Val Asp Thr Thr Val Val Glu Pro Asn Glu Pro Val Asn Lys Arg 560 565 570 575	7142
gcc cgt acg ccg agt cca gcc cca gtc gat caa gat ttg ccc gaa cca Ala Arg Thr Pro Ser Pro Ala Pro Val Asp Gln Asp Leu Pro Glu Pro 580 585 590	7190
aaa cca gag ccc gag tct g cag Lys Pro Glu Pro Glu Ser 595	7212

<210> SEQ ID NO 138

<211> LENGTH: 58

<212> TYPE: PRT

<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 138

Leu Gln Gln Tyr Phe Tyr Ser His Leu Val Asn Gln Thr Glu Ala Arg 1 5 10 15
Pro Asp Asp Tyr Glu Ala Glu His Leu Ser Ala Ala Arg Glu Lys Val 20 25 30
Asn Leu Gln Asn Cys Gly Ala Arg Gln Gln Asn Ala Leu Pro Leu Gly 35 40 45
His Ile Gly Pro Arg Asn Ser Ala Glu Pro 50 55

<210> SEQ ID NO 139

<211> LENGTH: 78

<212> TYPE: PRT

<213> ORGANISM: mosquito baculovirus

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<400> SEQUENCE: 139

```

Met Cys Thr Ile Tyr Arg Ser Ala Leu Lys Lys Thr Thr Thr Met
 1           5          10          15

Thr Val Asp Arg Arg Gly Pro Arg Ser Cys Asn Pro Pro Ser Glu Lys
 20          25          30

Thr Ile Ala Arg Pro Thr Thr Ser Leu Gln Ser Gln Arg Cys Ser Ile
 35          40          45

Pro Ser Ser Glu Ser Ile Thr Ile Lys Arg Ser Thr Val Gln Asn Lys
 50          55          60

Tyr Thr Leu Ile Asn Phe Ile Tyr Ile Val Tyr Phe Thr Gly
 65          70          75

```

<210> SEQ ID NO 140

<211> LENGTH: 124

<212> TYPE: PRT

<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 140

```

Met Leu Gly Ile Val Gly Ala Pro Val Ile Leu Gln Ile Leu Arg Ser
 1           5          10          15

Val Gln Val Asn Ile Leu Phe Arg Val Gln His Glu Ser Asp Gln Lys
 20          25          30

Arg Phe Asn Val Ala Asn Phe Thr Ala Arg Val His Arg Glu Leu Val
 35          40          45

His Val Arg Ser Ser Val Thr Val Gln Leu Gly Leu Gln Pro Val Ile
 50          55          60

Leu Val Ile Ala Ala Asn Cys Val Leu Glu Arg Val Arg Ala Lys Leu
 65          70          75          80

Glu Ile Leu Glu Gly Ser Trp Val Glu Leu His Ser Glu Arg His Tyr
 85          90          95

Trp Ala Asn Val Trp Val Lys Met Trp Gly Ala Leu Tyr Ile Asn Phe
100          105         110

Leu Ala Ile Ser Ala Ala Ser Val Ala Met Ser Ala
115          120

```

<210> SEQ ID NO 141

<211> LENGTH: 51

<212> TYPE: PRT

<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 141

```

Met Leu Ala Ala Pro Pro Leu Arg Ala His Val Arg Tyr Gly Thr Arg
 1           5          10          15

Pro Gly Arg Ser Ser Pro Thr Lys Leu Gly Pro Arg Lys Pro Val Pro
 20          25          30

Ile Arg Leu Glu Ala Gln Leu Val Arg Pro Phe Gly Leu Tyr Phe Glu
 35          40          45

Pro Gly Phe
 50

```

<210> SEQ ID NO 142

<211> LENGTH: 52

<212> TYPE: PRT

<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 142

```

Met Phe Ser Leu Lys Ser Leu Lys Ile Phe Ala Ile Phe Ser Cys Ser

```

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1	5	10	15
Lys His Pro Ser Ala Ser Trp Ser Val Leu Ala Trp Ser Thr Pro Arg			
20	25	30	
Leu Arg Leu Leu Arg Ala Ile Glu Tyr Gly Thr Val Ser Arg Tyr Trp			
35	40	45	
Val Arg Ser Thr			
50			

<210> SEQ ID NO 143
<211> LENGTH: 80
<212> TYPE: PRT
<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 143

Met Asp Ala Phe Thr Glu Thr Phe Leu Arg Gln Arg Val Ile Ile Asn			
1	5	10	15
Pro Glu Thr Lys Glu Ile Glu Val Arg Ala Val Cys Ser Asp Gly Val			
20	25	30	
Gly Tyr Thr Tyr Phe Thr Val Gly Gln Met Pro His Pro Val Thr Glu			
35	40	45	
Arg Asp Val Ser Gly Gly Ser Ser Asn Lys Ile Pro Ser Arg Ser Arg			
50	55	60	
Gly Ser Ala Glu Pro Leu Ser Gly Ala Cys Gly Tyr Lys Asn Gln Val			
65	70	75	80

<210> SEQ ID NO 144
<211> LENGTH: 154
<212> TYPE: PRT
<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 144

Leu Phe Asp Thr Thr Met Gln Phe Glu Ile Glu Ile Arg Asn Gly Asn			
1	5	10	15
Gln Leu Tyr Ser Ser Arg Asn Gln Leu Ile Leu Pro Gly Leu Thr Asp			
20	25	30	
Val Tyr Tyr His Tyr Val Ser Thr Ser Gly Pro Phe Gly Glu Asp His			
35	40	45	
Pro His Asp Ile Lys Leu His Thr Thr Val His Asn Tyr Asn Pro Asn			
50	55	60	
Leu Ala Val Phe Val Ile Gln Arg Glu Gly Thr Glu Leu Asn Lys Ile			
65	70	75	80
Ala Phe Arg Leu Gln Val Tyr Val Leu Lys Ala Thr Thr Phe Gly Ala			
85	90	95	
Gly Glu His Ile Ala Glu Val Asn Phe Ile Lys Pro Lys Gly Cys Gly			
100	105	110	
Asp Gly Lys Arg Ser Val Asp Thr Thr Val Val Glu Pro Asn Glu Pro			
115	120	125	
Val Asn Lys Arg Ala Arg Thr Pro Ser Pro Ala Pro Val Asp Gln Asp			
130	135	140	
Leu Pro Glu Pro Lys Pro Glu Pro Glu Ser			
145	150		

<210> SEQ ID NO 145
<211> LENGTH: 3997
<212> TYPE: DNA
<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 145

-continued

ctgcagcgat agttccatg aactcatcaa gctgaaacct accatggcc ttggctccc	60
ccagtagttc ctgcggaaag tcgttgaaga aatcttcgc ggtttgctcc attactctcc	120
tccgaagaca gcggccccgt cgcaactcgta tttagcaatc gtttccaatt tgatgtcgta	180
ggctaccttg gcaatacacgt tcggcaattt cgatcgcatg aggccgcggaa aatcatcgcc	240
gaccgatag ctgcgcacgt cgctgacgac aaaacgcggt tcatcgtagt caggagccgg	300
cgcgtagccg tgcgttgcgaa acttctggtc aaaggccctca acggccctctg ctttgtcgag	360
ctgcgcctgg acggcggtga caagctcggtt gagcgagccg gcacctaccg catcagccag	420
attgctcgc cggttacacgc gcaggaacag tgcgtcggttcc agggattcga gctggcttcc	480
cgaagaaatg cggatgtgc tccgttccgc gcccggagagc gatttgaccc cgacagccgt	540
gttaccgaag atgaaatcct gatgtgaccg ttccggacca agccaggott caacgacggc	600
attgctcggc atttcccgat cgatcgttcc cgtcagaaaag acgatttcgg cgaaggaggcc	660
tcgaacatct tcggggacaa gatgtgact tcggcccgag agaaactct tcacaacgacg	720
gatgtgcgc aacgagactg ccagagagcc ggccgaatcg gtggcgact ccaacgcgaa	780
tgcaagggtt cggcagatc cctcgaaaatg atcgcgtatca acctgtctt caagagccgg	840
gacttaggtt tgctgcccgtt gatctccggc acgaagatcg acatcgacac cgttcactgt	900
gaccgcgttc ttccggactt gggctgtgt gtcgcccgtga agtccacaa tgaacaggca	960
ggcaccgcgtg gcatcgcgtc cccagaaaaca ggttacggcc gttttcacccg caacctggcg	1020
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agtccctcctc ctgcgttccatgc tccgtccat agccctgcat ctgcgttccatgc cagacccgt	1140
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gatcgcccccc gtcacggcat cggcccttggg ttccagactg tgaatcatga ggaggggtct	1260
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cagcagaaca tccgcacgc gacgttctgt cgccatccgt tcgagatagc tcaccacatc	1560
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cggcatcgcg tagttggcga gaaccgcctc cctgatcttc ttctccctga ggctcaggaa	2400
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cttgctggcc tgcgcgcga ggtccggat ggccgcgtgc atgatgaact cgtcgagtgc	2520
gcgatggagg ctggcaggca gctcatggac aggatcatcg cgtttgcg agtagggaaat	2580
gagatcctcg caatcatcga tcggcctgtat gatcgattcg ctggcgcct cattcaggaa	2640
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gaaaaagctct tcctgcacat catgccata ggcatctgga ttgatgaaga tttggcgaa	2760
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gaagattgca gcaatctgtc ttgccttttc ctccacactga tcgcgcgtcg gctttccgc	3660
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aatgctcatg caaaggccctc gttgtatgtt tttccgcata gatccatctg gccatcgaa	3780
agatgcgtgg agcgcacatcg ctgaagaaaa gcttcgtatcg cggccggccg gtcgcgtac	3840
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ttgatctgcg cgggttgcgttgc gcaatgttgc gatccatcgatcc gatcgatgttgc	3960
gcaaccgaat caagcagcgt ggcagcagg tctgcag	3997

<210> SEQ ID NO 146
<211> LENGTH: 3997
<212> TYPE: DNA
<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 146

ctgcagacatc gctgcgcacg ctgttgcattt cgggttgcgtc ctcactgcgg gtcgagatga	60
tctattccga ctactcgact caccgcgcg agatcaatca acgatcggtt gatgaaagcc	120
agaccatggaa ggcgttgcgttgc aagttgcgttgc cggcgcgggg ccggggcgatg	180
cgaaagcttt tcttcgtatcgatc gtcgcgttca cgcacatctt cgtatggccatcg atggatctgg	240
ccgaaaaattt catcaacgatc gcttgcgttgc gacatggccatcg aagaacgaaa	300
cattgccaac ggcgttgcgttgc caacatggccatcg gaaacgcggaa cgcgcgtatca	360
ggtggaggaa aaggcaagac agattgcgttgc aatcttcgttgc tatgcggggag acctccgc	420
cattgtcacc caagctatgg aatcggttgc gacccgcgttgc ggagcaggaa ttcttgcgttgc	480

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tgtatgtcaat	gcgaagcatg	acgtacaatg	ggttcacaag	cgcgaggacg	tcacttggac	540
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gtcgctgagc	gatgtgacca	ctcgattct	tggtcacett	caggatccac	tgagcgaagg	660
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ccgatcgagt	gaccggagg	atcgccgcaa	catcgccgtc	ggtctcgttt	cgggatatcc	900
gcatccggca	acgctcacca	acatcaacga	ggacttcaac	aagaatacag	cagccaaagag	960
tggcttgaag	atcaacgact	tcagcaagcc	gatcatcctg	atcatcaaga	agaacgtcac	1020
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cagcaagagt	gacgagggtgc	tcgactacac	ccggtaacg	aaggaaggca	tccggctgac	1860
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gatcgcgacg	aaggctccgc	ttggggatgt	tctgctgtt	tccctcg	gtgggtcg	2520
tggcgaacgc	ccattcacgt	tggaaatca	ggtgcgtgtc	gtcggtgggg	atcagccgaa	2580
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gctcagcgc	gagcaacgcg	ctgaggccag	aacggtcgt	ggcgcacgac	acggctcg	2700
ggcggtatcc	gacacacatt	accggatgt	gaggaacaga	ccctcctca	tgattcaca	2760
tctggaaaccc	aaggcgatcg	ccgtgacggg	ccgcgtatcg	gccttggca	ttagctccc	2820

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ttacggggac tactcgacga ccatcaatgt ctgcgtcaaca aggtctggct tcagcagatg	2880
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cgtaccctgt ttctggggac gcgatgccag cggtgcctgc ctgttcattg tggagcttca	3060
cggcgaccac acagcccagt accggaagaa cgcggtcaca gtgaacggtg tcgatgtcga	3120
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tccggaacgg tcacatcagg atttcattt cggtaacacg gctgtcgagg tcaaatcgct	3480
ctcgccgcgc gaacggagca gcacccgcatttccggaa gaccagctcg aatccctgaa	3540
cgacgcactg ttcctgcgcg tggccggcttggc gagcaatctg gtcgtatgcgg taggtgcccc	3600
ctcgctcaac gagcttgtca ccgcgttcca ggccgcagtc gacaaggcag aggccgttga	3660
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cgcttttgcg tgcacgcgcg tggccgcgttggc gatgttttc cgccgcctcat	3780
cgatcgcaat ttcggccacag gtattgccaa ggtggccatc gacatcaaataat tggaaacgat	3840
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gaagatttct tccacgactt ccggcaggaa ctactggccgg gacccaaaggc aaatggtagg	3960
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<210> SEQ ID NO 147

<211> LENGTH: 705

<212> TYPE: DNA

<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 147

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ttgaaaactg acgaccccgaa gttggccaaac tttgtgctca acgtgtccgtt ggtcacctca	180
atgttcttct tcggtaccga aaacattaaa gtttaccaca cgggcaacga cggcatccac	240
atttggctca accggccaa ctccccgggt gactcgagcg cccaaatgcg cggattctac	300
ctcgccgcca tgcagctacc caaagggtgag gaggaactac acgagctggt gcgaccacc	360
gagtgcaggt tggccgcgcg cggccactgc tggccaatcg attgcaagcc caagatgcgc	420
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gctctcgct gcaacgaaac ctatatgaac gaaatgacat cgattatacg caacaaccgg	540
gacgtgggtga gcacccgtcac cgacgtgtgg agactctttt ggccgcccatt agatgcgggc	600
ctgtttcaat cgccgacttag actctggccgt gcacccctca gttaccactt gaaaggccgg	660
cggcttcgc gtcgtattga ctggatgaa tattttaaaa atgat	705

<210> SEQ ID NO 148

<211> LENGTH: 1032

<212> TYPE: DNA

<213> ORGANISM: mosquito baculovirus

<400> SEQUENCE: 148

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atgcgcctcg aagatgaacc gagcgcctcgag gaccagatga ttgattttat aaacaataac	60
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gccctcatga agaaggccat ggtgcggtaat atccccatgc tgcaagccgc cgcaatacg	180
ttcgggtgaag gcttgacacg taaaatggtc tcggaggcgat ttctgtgtct catgttttagc	240
cgcataaaacc agatggccgt gcagctgacc ggcgccttag cgaaggcaat tgacgcgtt	300
ggtgcgatgg ccagttcggt gatttggaaat gtgttgatat ttttcgtcg acggatata	360
attctcatgt tctgggaccc gtacggttac agcaacatgt ttccgcccga gtttctggc	420
gatttgacgc tcaactttctt gtccggcgat ttccgagcaaa cgggtacgcg aaacgtatac	480
gaaatgatac cccaaagcgta cgactctatg gtgaaagggtg gtgaggagga tggactctac	540
ctaacattttgc cccgcctaca atacgtgagc catatggagg tgaactcgaa cgggcagtt	600
ttgctgctac gaaacagtaa cccaaatcaag caggaggaac ttgagccgca caacctcacy	660
gtggccctct tcggcgctat aaacctgcag agttatgggg atcttaagcg gcatatggcc	720
agcgcacaacc gggcccttcgg tatagacccc gaaacgttgc agcaagtggc cccgtggaga	780
gatagacccg ggacagtaat ttccagctggc gtccttagtt cgcttgggtg ctgtttgacc	840
gggagtcaac ttttcagcac aaaagcgccc gatctagcta cggtgggtct cattgttaatt	900
ctgggtggcca tagtataat cgtgtaccaa ctcgaccgta taacacccc gccccgactt	960
gccatcgtaa agcatgaaga gaacgagaaa aatcgcgtcg gccaacgcgtt cgccggactg	1020
cttagacgtg ct	1032

We claim:

1. A method for the in vitro propagation of a mosquito baculovirus comprising infecting a culture of mosquito cells with a baculovirus, growing the cells in culture medium containing at least 1 mM of a divalent cation selected from the group consisting of: magnesium, cobalt, strontium, and nickel; and a chelator binder that selectively reduces the effective calcium ion concentration below about 1 mM until inclusion bodies are detected in the cells, and harvesting the virus from the cells.

2. The baculovirus of claim 1, wherein the baculovirus has been engineered to express an insect-antagonistic gene.

3. The baculovirus of claim 2, wherein the insect-antagonistic gene is selected from the group consisting of: toxins, insect hormones, insect hormone mimics, and sterilization peptides.

4. An isolated mosquito-infecting baculovirus having the following characteristics:

- (a) nuclear occlusion bodies, globular in shape, diameter approximately 400 nm, each containing between about 1–8 rod-shaped virions, approximately 200×40 nm;
- (b) nuclear occlusion bodies with no surrounding membrane and with a density of approximately 1.14–1.18 g/ml which agglutinate upon freezing; and
- (c) infectious in *Culex quinquefasciatus* and *Culex nigripalpus*.

5. The baculovirus of claim 4, wherein the baculovirus has been engineered to express an insect-antagonistic gene.

6. The baculovirus of claim 5, wherein the insect-antagonistic gene is selected from the group consisting of: toxins, insect hormones, insect hormone mimics, and sterilization peptides.

7. A method for controlling mosquitos comprising the step of applying a mosquito-controlling amount of the baculovirus of claim 4 to a habitat.

35 8. The method of claim 7 wherein said habitat is a mosquito breeding area.

9. The method of claim 7, wherein the mosquitos are members of Culicidae.

10. An insecticidal composition consisting essentially of:
(a) a baculovirus effective for producing a lethal or debilitating infection in an insect; and
(b) at least about 1 mM of a divalent cation selected from the group consisting of: magnesium, cobalt, strontium, and nickel.

11. The composition of claim 10, further comprising an insecticidal composition-suitable carrier.

12. The composition of claim 10, wherein the divalent cation is magnesium.

13. The composition of claim 12 wherein the concentration of magnesium is at least about 5 mM.

14. The insecticidal composition of claim 13, wherein the composition is a mosquito larvacial composition.

15. The composition of claim 14, wherein the baculovirus is CuniNPV.

16. The composition of claim 14, wherein the baculovirus is selected from the group consisting of nuclear polyhedrosis viruses that infect *Culex*, *Aedes*, *Anopheles*, *Psorophora*, *Uranotaenia*, and *Wyeomyia* mosquito species.

55 17. A method for controlling mosquitos comprising the step of applying a mosquito-controlling amount of the composition of claim 10 to a habitat for said mosquito.

18. The method of claim 17, wherein the mosquitos are members of Culicidae.

19. The method of claim 17, wherein said habitat is a mosquito breeding area.

20. An insecticidal composition comprising:
(a) a baculovirus effective for producing a lethal or debilitating infection in an insect;

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- (b) at least about 1 mM of a divalent cation selected from the group consisting of: magnesium, cobalt, strontium, and nickel; and
 - (c) a chelator or binder that selectively reduces the effective calcium concentration below about 1 mM.
21. The composition of claim 20, further comprising an insecticidal composition-suitable carrier.
22. The composition of claim 20 wherein the divalent cation is magnesium.
23. The composition of claim 22 wherein the concentration of magnesium is at least about 5 mM.
24. The composition of claim 23, wherein the composition is a mosquito larvacial composition.

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- 5 25. The composition of claim 24, wherein the baculovirus is CuniNPV.
- 26. The composition of claim 24, wherein the baculovirus is selected from the group consisting of nuclear polyhedrosis viruses that infect Culex, Aedes, Anopheles, Psorophora, Uranotaenia, and Wyeomyia mosquito species.
- 10 27. An isolated nucleic acid comprising a nucleotide sequence set forth in SEQ ID NO: 83.
- 28. A cell containing a nucleic acid of claim 27.
- 29. The cell of claim 28 wherein the cell is from an insect.

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